

FIGURE 1

ACTGCACCTCGGTTCTATCGATTGAATTCCCGGGGATCCTCTAGAGATCCCTCGACCTCGA
CCCACGCGTCCGGGCGGAGCAGCACGGCCGAGGACCTGGAGCTCCGGCTCGCTCTTCCCG
CAGCGCTACCCGCCATGCGCCTGCCGCGCCGGCCGCGCTGGGGCTCCTGCCGCTTCTGCTG
CTGTGCGCGCCGCGCGGAGGCCGCCAAGAAGCCGACGCCCTGCCACCGGTGCGCGGGGCT
GGTGAGACAAGTTTAACCAGGGGATGGTGACACCGCAAAGAAGAACTTTGGCGGCGGGAACA
CGGCTTGGGAGGAAAAGACGCTGTCCAAGTACGAGTCCAGCGAGATTTCGCTGCTGGAGATC
CTGGAGGGGCTGTGCGAGAGCAGCGACTTCGAATGCAATCAGATGCTAGAGGCGCAGGAGGA
GCACCTGGAGGCCTGGTGGCTGCAGCTGAAGAGCGAATATCCTGACTTATTTCAGTGGTTTT
GTGTGAAGACACTGAAAGTGTGCTGCTCTCCAGGAACCTACGGTCCCGACTGTCTCGCATGC
CAGGGCGGATCCAGAGGCCCTGCAGCGGGAATGGCCACTGCAGCGGAGATGGGAGCAGACA
GGGCGACGGGTCTGCCGTTGCCACATGGGGTACCAGGGCCCGCTGTGCACTGACTGCATGG
ACGGCTACTTCAGCTCGCTCCGGAACGAGACCCACAGCATCTGCACAGCCTGTGACGAGTCC
TGCAAGACGTGCTCGGCCCTGACCAACAGAGACTGCGGCGAGTGTGAAGTGGGCTGGGTGCT
GGACGAGGGCGCCTGTGTGGATGTGGACGAGTGTGCGGCCGAGCCGCCCTCCCTGCAGCGCTG
CGCAGTTCTGTGAAGAACGCCAACGGCTCCTACACGTGCGAAGAGTGTGACTCCAGCTGTGTG
GGCTGCACAGGGGAAGGCCCAGGAACTGTAAAGAGTGTATCTCTGGCTACGCGAGGGAGCA
CGGACAGTGTGCAGATGTGGACGAGTGTCTACTAGCAGAAAAAACCTGTGTGAGGAAAAACG
AAAACCTGCTACAATACTCCAGGGAGCTACGTCTGTGTGTGTCTGACGGCTTCGAAGAAACG
GAAGATGCCTGTGTGCCCGCGGAGAGGCTGAAGCCACAGAAGGAGAAAGCCCGACACAGCT
GCCCTCCCGCGAAGACCTGTAATGTGCCGGACTTACCCTTTAAATTATTTCAGAAGGATGTCC
CGTGGAATAATGTGGCCCTGAGGATGCCGCTCTCTGCAGTGGACAGCGCGGGGAGAGGCTGC
CTGCTCTCTAACGGTTGATTCTCATTTGTCCCTTAAACAGCTGCATTTCTTGGTTGTTCTTA
AACAGACTTGTATATTTTGATACAGTTCCTTGTAATAAAATTGACCATTGTAGGTAATCAGG
AGGAAAAAAAAAAAAAAAAAAAAAGGGCGGCCGCGACTCTAGAGTCGACCTGCAGAAGC
TTGGCCCGCATGGCCCAACTTGTTTATTGCAGCTTATAATGGTTACAAATAAAGCAATAGCA
TCACAAATTTACAAATAAAGCATTTTTTCTACTGCATTCTAGTTGTGGTTTGTCCAAACTC
ATCAATGTATCTTATCATGTCTGGATCGGGAATTAATTCGCGCAGCACCATGCGCTGAAAT
AACCTCTGAAAGAGGAACCTTGTTAGGTACCTTCTGAGGCGGAAAGAACCAGCTGTGGAATG
TGTGTCAAGTTAGGTTGTGGAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAGCATGC
ATCTCAATTAGTCAGCAACCCAGTTTT

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FIGURE 2

><subunit 1 of 1, 353 aa, 0 stop
><MW: 38192, pI: 4.53, NX(S/T): 2
MRLPRAALGLLPLLLLLPPAPEAAKKPTPCHRCRGLVDKFNQGMVD TAKNPGGGNTAWEKTL SKYESS EIRL
LEILEGLCESSDFECNQMLEAQBEHLEAWWLQKSEYD LFEWFCVKTLKVC CSPGT YGPDCLACQGG SQRPCSG
NGHCSGDGSRGD GSCRC HMGYQG PLCTDCMDGYFSSLRNETHS ICTACDESKCTCSGLTNRDCGEC EVGWV LDE
GACVDVDECAAEPPPCSA AQFCKNANGSYTC EECDS SCVGCTGEGPGNCKE CISGYAREHGQ CADVDECS LAEKT
CVRKNENCYNTPGSYVVCVCPDGF EETEDACVPPAEAEATEGESPTQLPSREDL

Signal peptide:

amino acids 1-24

N-glycosylation sites.

amino acids 190-194 and 251-255

Glycosaminoglycan attachment sites.

amino acids 149-153 and 155-159

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 26-30

Casein kinase II phosphorylation sites.

amino acids 58-62, 66-70, 86-90, 197-201, 210-214, 255-259, 295-299, 339-343
and 349-353

Tyrosine kinase phosphorylation site.

amino acids 303-310

N-myristoylation sites.

amino acids 44-50, 54-60, 55-61, 81-87, 150-156, 158-164, 164-170, 252-258 and
313-319

Aspartic acid and asparagine hydroxylation site.

amino acids 308-320

EGF-like domain cysteine pattern signature.

amino acids 166-178

Leucine zipper pattern.

amino acids 94-116

FIGURE 3

CAGGTCCAACCTGCACCTCGGTTCTATCGATTGAATCCCCGGGGATCCTCTAGAGATCCCTC
GACCTCGACCCACGCGTCCGCCAGGCCGGGAGGCGACGCGCCAGCCGCTCTAAACGGGAACA
GCCCTGGCTGAGGGAGCTGCAGCGCAGCAGAGTATCTGACGGCCAGGTTGCGTAGGTGCG
GCACGAGGAGTTTTCGCCGAGCGAGGAGGTCTTGAGCAGC**AT**GGCCCCGAGGAGCGCCTTC
CCTGCCGCCGCGCTCTGGCTCTGGAGCATCTCTGTGCTGCTGGCACTGCGGGCGGAGGC
CGGGCCGCCGAGGAGGAGAGCCTGTACTATGGATCGATGCTCACCAGGCAAGAGTACTCA
TAGGATTTTGAAGAAGATATCTGATTGTTTCAGAGGGGAAAATGCGACCTTTTACACATGAT
TTCAGAAAAGCGCAACAGAGAATGCCAGCTATTCCGTCAATATCCATTCCATGAATTTTAC
CTGGCAAGCTGCAGGGCAGGCAGAATACTTCTATGAATTCCTGTCTTGGCTCCCTGGGATA
AAGGCATCATGGCAGATCCAACCGTCAATGTCCCTCTGCTGGGAACAGTGCCTCACAAGGCA
TCAGTTGTTCAAGTTGGTTTCCCATGTCTTGGAACAACAGGATGGGGTGGCAGCATTGGAAGT
GGATGTGATTGTTATGAATTCGAAGGCAACACCATTCTCCAAACACCTCAAATGCTATCT
TCTTTAAACATGTCAACAGCTGAGTGCCAGGCCGGTGCCGAAATGGAGGCTTTTGTAAT
GAAAGACGCATCTGCGAGTGTCTGTATGGGTTCCACGGACCTCACTGTGAGAAAAGCCCTTG
TACCCACGATGTATGAATGGTGGACTTTGTGTGACTCCTGGTTTCTGCATCTGCCACCTG
GATTCTATGGAGTGAACCTGTGACAAAGCAAACCTGCTCAACACCTGCTTAATGGAGGGACC
TGTTTCTACCTCGGAAAATGTATTTGCCCTCCAGGACTAGAGGGAGAGCAGTGTGAATCAG
CAAAATGCCACAACCTGTGCAAAATGGAGGTAAATGCATTGGTAAAAGCAAAATGTAAGTGTT
CCAAAGGTTACCAAGGAGACCTCTGTTCAAAGCCTGTCTGCGAGCCTGGCTGTGGTGCACAT
GGAACCTGCCATGAACCAACAAATGCCAATGTCAAGAAGGTTGGCATGGAAGACATGCAA
TAAAGGTACGAAGCCAGCCTCATACATGCCCTGAGGCCAGCAGCGCGGGATCCACCTGAATCCAATTACATCTGG
TGAACTCCGACATCTGAAACGTTTAAAGTTACACCAAGTTCATAGCCTTTGTTAAACCTTTCA
TGTGTTGAATGTTCAATAATGTTCAATTACACTTAAGAATACTGGCCTGAATTTTATTAGCT
TCATTATAAATCACTGAGCTGATATTTACTCTTCTTTTAAAGTTTCTAAGTACGTCTGTAG
CATGATGGTATAGATTTTCTGTTTCAGTGCTTTGGGACAGATTTTATATTATGTCAATTGA
TCAGGTTAAAAATTTTCAGTGTGTAGTTGGCAGATATTTTCAAATTAACAATGCATTATAGGT
GTCTGGGGGCGAGGGGAACATCAGAAAGGTTAAATGGGCAAAAATGCGTAAAGTACAGAAT
TTGGATGGTGCAGTTAATGTTGAAGTTACAGCATTTTCAAGTTTATTGTGATATTTAGAT
GTTTGTGTTACATTTTAAAAAATGCTCTTAATTTTAAACTCTCAATACAATATATTTTGACC
TTACCATTATTCCAGAGATTAGTATTAATAAAAAAAAAAATACACTGTGGTAGTGGCATT
AAACAATAATAATATTCTAAACACAATGAAATAGGAATATAATGTATGAACCTTTTGCAT
TGGCTTGAAGCAATATAATATATTGTAACAAAAACACAGCTCTTACCTAATAAACATTTTAT
ACTGTTTGTATGTATAAAATAAGGTGCTGCTTTAGTTTTTTGGAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAGGCGCGCGCACTTAGAGTCGACCTGCAGAAGCTTGGC
CGCCATGCCCCAAGCTTTTATTGCAGCTTATAATG

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100100-250000

FIGURE 4

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA33094
><subunit 1 of 1, 379 aa, 0 stop
><MW: 41528, pI: 7.97, NX(S/T): 2
MARRSAFPAAALWLWSILLCLLALRAEAGPPQEESLYLWIDAHQARVLIGFEEDILIVSEGK
MAPFTHDFRKAQQRMPAIPVNIHSMNFTWQAAGQAEYFYEFSLRSLDKGIMADPTVNVPLL
GTVPHKASVVQVGFPCLGKQDGVAAFEVDVIVMNSEGNITLQTPQNAIFFKTCQQAECPGGC
RNGGFCNERRICECPDGFHGHPCKEALCTPRCMNGGLCVTPGFCICPPGFYGVNCDKANCST
TCFNGGTCTFYPGKCICPPGLEGEQCEISKCPQPCRNGGKIGKSKCKCSKGYQGDLCSKPVC
EPGCGAHGTCHEPNKCQCQEGWHGRHCNKRYEASLIHALRPAGAQLRQHTPSLKKAEERRDP
PESNYIW

Signal peptide:

amino acids 1-28

N-glycosylation site.

amino acids 88-92, 245-249

Casein kinase II phosphorylation site.

amino acids 319-323

Tyrosine kinase phosphorylation site.

amino acids 370-378

N-myristoylation sites.

amino acids 184-190, 185-191, 189-195, 315-321

ATP/GTP-binding site motif A (P-loop).

amino acids 285-293

EGF-like domain cysteine pattern signature.

amino acids 198-210, 230-242, 262-274, 294-306, 326-338

FIGURE 5

CGGACGCGTGGGCGTCCGGCGGTGCGAGAGCCAGGAGGCGGAGGCGCGGGGCCAGCCTGGG
CCCCAGCCCCACACCTTACCAGGGGCCAGGAGCCACCATGTGGGCGATGTCCACTGGGGCTAC
TGCTGTTGCTGCCGCTGGCTGGCCACTTGGCTCTGGGTGCCAGCAGGGTCGTGGGCGCCGG
GAGCTAGCACCGGGTCTGCACCTGCGGGGCATCCGGGACGCGGGAGGCGGGTACTGCCAGGA
GCAGGACCTGTGCTGCCGCGGGCGGTGCCGACGACTGTGCCCTGCCCTACCTGGGCGCCATCT
GTTACTGTGACCTCTTCTGCAACCGCACGGTCTCCGACTGCTGCCCTGACTTCTGGGACTTC
TGCTCTGGCGTGCCACCCCCCTTTTCCCCGATCCAAGGATGTATGCATGGAGGTCTGTATCTA
TCCAGTCTTGGGAACGTACTTGGGACAACCTGTAACCGTTGCACCTGCCAGGAGAACAGGCAGT
GGCATGTGTGATCCAGACATGATCAAAGCCATCAACCAGGGCAACTATGGCTGGCAGGCCTGG
GAACCACAGCGCTTCTGGGGCATGACCTGGATTGAGGGCATTTCGTACCGCTGGGCACCA
TCCGCCATCTTCTCGGTATGAACATGCATGAAATTTATACAGTGTCTGAACCCAGGGGAG
GTGCTTCCACAGCCTTCGAGGGCTCTGAGAAGTGGCCCAACCTGATTATGAGCCTCTTGA
CCAAGGCAACTGTGCAGGCTCTTGGGCTTCTCCACAGCAGCTGTGGCATCCGATCGTGTCT
CAATCCATTCTCTGGGACACATGACGCTGTCTGTGCGCCCAAGACCTGCTGTCTTGTGAC
ACCCACAGCAGCAGGGCTCGCCGGTGGGCGTCTCGATGGTGCCTGGTGGTTCCTGCGCTCG
CCGAGGGGTGGTGTCTGACCACTGCTACCCCTTCTCGGGCCGTGAACGAGACGAGGCTGGCC
CTGCGCCCCCTGTATGATGCACAGCCGAGCCATGGGTCTGGGGCAAGCGCCAGGCCACTGCC
CACTGCCCAACAGCTATGTTAATAAACAATGACATCTACCAGGTCACCTCTGTCTACCGCCT
CGGCTCCAACGACAAGGAGATCATGAAGGAGCTGATGGAGAATGCCCTGTCCAAGCCCTCA
TGGAGGTGCATGAGGACTTCTTCTATACAAGGGAGGCATCTACAGCCACACGCCAGTGAGC
CTTGGGAGCCAGAGAGATACCGCGGCATGGGACCACTCAGTCAAGATCACAGGATGGGG
AGAGGAGACGCTGCCAGATGGAAGGACGCTCAAATACTGGACTGCGGCCAACTCTGGGGCC
CAGCCTGGGGCGAGAGGGGCCACTTCCGATCGTGC CGCGCGTCAATGAGTGCAGATCGAG
AGCTTCGTGCTGGCGTCTGGGGCCGCGTGGGCATGGAGGACATGGGTCTACTGAGGCTG
CGGGCACACGCGGGGTCCGGCCTGGGATCCAGGCTAAGGGCCGGCGGAAGAGGCCCAATG
GGGCGGTGACCCAGCCTCGCCGACAGAGCCCGGGCGCAGGCGGGCGCCAGGGCGCTAAT
CCCGCGCGGGTTCCGCTGACGCGAGCGCCCCGCTGGGAGCCGCGGGCAGGCGAGACTGGCG
GAGCCCCAGACCTCCAGTGGGGACGGGGCAGGGCTTGGCTGGGAAGAGCACAGCTGCAG
ATCCAGGCCTCTGGCGCCCCCACTCAAGACTACCAAAGCCAGGACACCTCAAGTCTCCAGC
CCCAATACCCACCCCAATCCCGTATTCTTTTTTTTTTTTTTTTATAGACAGGTCTTGCTCCG
TTGCCAGGTTGGAGTGCACTGGCCATCAGGGCTCACTGTAACCTCCGACTCCTGGGTTCA
AGTGACCTCCACCTCAGCCTCTCAAGTAGCTGGGACTACAGGTGCACCAACACACCTGGC
TAATTTTTGTATTTTTGTAAAGAGGGGGTCTCACTGTGTGCCAGGCTGGTTTCGAAC
CTTGGGCTCAAGCGTCCACTGCTCCGCTCCCAAAGTCTGGGATGCAAGGATGAGGC
ATGCACCCAGCCCTGTATTCTTATTCTTCAGATATTTATTTTTCTTTTCACTGTTTTAAAA
TAAACCAGGATTTGATAAAAAAAA

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FIGURE 6

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA33223

><subunit 1 of 1, 164 aa, 1 stop

><MW: 18359, pI: 7.45, NX(S/T): 1

MWRCPLGLLLLLPLAGHLALGAQQGRGRRELAPGLHLRGIRDAGGRYCQEQLCCRGRADDC
ALPYLGAICYCDLFCNRTVSDCCPDFWDFCLGVPPFPPIQGCMHGGRIYPVLGTYWDNCNR
CTCQENRQWHGGSRHDQSHQPGQLWLAGWEPQRLLGHDPG

N-glycosylation site.

amino acids 78-82, 161-165

Casein kinase II phosphorylation site.

amino acids 80-84, 117-121, 126-130, 169-173, 205-209, 296-300,
411-415

N-myristoylation site.

amino acids 21-27, 39-45, 44-50, 104-110, 160-164, 224-230,
269-275, 378-384, 442-448

Amidation site.

amino acids 26-30, 318-322

Eukaryotic thiol (cysteine) proteases histidine active site.

amino acids 398-409

FIGURE 7

AGGCTCCTTGGCCCTTTTCCACAGCAAGCTTNTGCNATCCCGATTGTTGTCTCAAATCCA
ATTCTCTTGGGACACATNAGCCTGTCTCTTTNGCCCCAGAACCTGCTGTCTTGTACACCCAC
CAGCAGCAGGGCTGCCGCGNTGGGCGTCTCGATGGTGCTGGTGGTTCCTGCGTCGCCGAGG
GNTGGTGTCTGACCACTGCTACCCCTTCTCGGGCCGTGAACGAGACGAGGCTGGCCCTGCGC
CCCCCTGTATGATGCACAGCCGAGCCATGGGTGCGGGCAAGCGCCAGGCCACTGCCCACTGC
CCCAACAGCTATGTTAATAACAATGACATCTACCAGGTCACTCCTGTCTACCGCCTCGGCTC
CAACGACAAGGAGATCATGAAGGAGCTGATGGAGAATGGCCCTGTCCAAGCCCTCATGGAGG
TGCATGAGGACTTCTTCTATACAAGGGAGGCATCTACAGCCACACGCCAGTGAGCCTTGGG
AGGCCAGAGAGATACCGCCGGCATGGGACCCACTCAG

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FIGURE 8

GCTGCTTGCCCTGTTGATGGCAGGCTTGGCCCTGCAGCCAGGCACTGCCCTGCTGTGCTACT
CCTGCAAAGCCCAGGTGAGCAACGAGGACTGCCTGCAGGTGGAGAACTGCACCCAGCTGGGG
GAGCAGTGCTGGACCGCGCGCATCCGCGCAGTTGGCCCTCTGACCGTCATCAGCAAAGGCTG
CAGCTTGAAGTGCCTGGATGACTCACAGGACTACTACGTGGGCAAGAAGAACATCACGTGCT
GTGACACCGACTTGTGCAACGCCAGCGGGGCCCATGCCCTGCAGCCGGCTGCCGCCATCCTT
GCGCTGCTCCCTGCACTCGGCCCTGCTGCTCTGGGGACCCGGCCAGCTATAGGCTCTGGGGGG
CCCCGCTGCAGCCCCACACTGGGTGTGGTGCCCCAGGCCCTCTGTGCCACTCCTCACAGACCTG
GCCCAGTGGGAGCCTGTCTGGTTCCTGAGGCACATCCTAACGCAAGTCTGACCATGTATGT
CTGCACCCCTGTCCCCACCCCTGACCCTCCCATGGCCCTCTCCAGGACTCCCACCCGGCAGA
TCAGCTCTAGTGACACAGATCCGCCTGCAGATGGCCCCCTCCAACCCCTCTCTGCTGCTGTTTC
CATGGCCCAGCATTCTCCACCCTTAACCCTGTGCTCAGGCACCTCTTCCCCCAGGAAGCCTT
CCCTGCCCCCCCCATCTATGACTTGAGCCAGGTCTGGTCCGTGGTGTCCCCCGCACCCAGCA
GGGGACAGGCACTCAGGAGGGCCAGTAAAGGCTGAGATGAAGTGGACTGAGTAGAACTGGA
GGACAAGAGTCGACGTGAGTTCTGGGAGTCTCCAGAGATGGGGCCTGGAGGCCTGGAGGAA
GGGGCCAGGCCTCACATTCTGTGGGGCTCCCTGAATGGCAGCCTGAGCACAGCGTAGGCCCTT
AATAAACACCTGTTGGATAAGCCAAAAAAA

FIGURE 9

MTHRTTTWARRTSRAVTPTCATPAGPMPCSRLLPPSLRCSLHSACCSGDPASYRLWGAPLQPT
LGVVVPQASVPLLLTDLAQWEPLVPEAHPNASLTMYVCTPVPHDPFPMALSRTPTRQISSDT
DPPADGPSNPLCCCFHGPAPFSTLNPVLRHLFPQEAFFAHPIYDLSQVWSVVSPAPSRGQALRRAQ

Signal peptide:

amino acids 1-47

N-glycosylation site.

amino acids 31-35, 74-78, 84-88

Casein kinase II phosphorylation site.

amino acids 22-26, 76-80

N-myristoylation site.

amino acids 56-60

Amidation site.

amino acids 70-74

Year	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100
1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100	

CCACACGCGTCCGAACCTCTCCAGCGATGGAGGAGCCGCCGCTGTGCCCCAACCTCACTCTGTG
GCTTACAGCTGCTGATTCTCTGCTGTCAAACCTAGTACGTGAGGGACCCAGGGCGCCATGACC
GACCAGCTGAGCAGGGCGGCAGATCCGCGAGTACCAACTCTACAGCAGGACCAGTGGCAAGCA
CGTGCAGGTCAACGGGGCGTCGCATCTCCGCCACCGCCGAGGACGGCAACAAGTTTGCCAAGG
TCATAGTGAGAGACGGACACGTTTGGCAGCCGGGTTTCGCATCAAAGGGGCTGAGAGTGAGAAG
TACATCTGTATGAAACAAGAGGGGCAAGCTCATCGGAAGCCACGCGGGAAGAGCAACAAGATG
CGTGTTTCACGGAGATCGTGTGGAGAACCACTATACGGCCTTCCAGAACGCCCGGCACGAGG
CTGTGTTTCATGGCCTTACGCGCGAGGGGCGGCCCGCGAGCTTCCCGCAGCCGCGCAGAAAC
CAGTCGAGGCCCCCACTTCACTAAGCGCCTCTACCAAGGCCAGCTGCCTTCCCCAACCCAGC
CGAGAAGCAGAAGCAGTTCGAGTTTGTGGGCTCCGCCCCACCCCGCGGACCAAGCGCACAG
GGCGGCCCCAGCCCCCTACGTTAGCTCTGGGAGGCGAGGGGCGAGCCCCCTGGGCGCGCTCCC
CACCCCTTTCCCTTCTTAATCCAAGGACTGGGCTGGGGTGGCGGGAGGGGAGCCAGATCCCC
GAGGGAGGACCTTGAGGGCCGCAAGCATCCGAGCCCCAGCTGGGAAGGGGCGAGCCGGTG
CCCCAGGGGCGGTGGGCACAGTGCCCCCTTCCCGACGGGTGGCAGGCCCTTGAGAGGAACT
GAGTGTCAACCCTGATCTCAGGCCACCAGCCTCTGCCGGCTCCAGCCGGGCTCCTGAAGCC
CGCTGAAAGGTACAGCGACTGAAGGCCTTGAGACAACCGTCTGGAGGTGGCTGTCTCTCAAA
TCTGCTTCTCGGATCTCCCTCAGTCTGCCCCAGCCCCAAACTCTCTGGGTAGACTGTA
GGAAGGCACTTTTGTTGTTTGTGTTTTCAGGAAAAAGAAAGGAGAGGAGAGGAAATAG
AGGGTTGTCCACTCTCTACATTTCACGACCCAGGCCTGCACCCCACTCCAGCCC
CGGAATAAAACCATTTTCCTGC

FIGURE 11

MGAARLLPNLTLCQLLLILCCQTQYVRDQGAMTDQLSRRQIREYQLYSRTSGKHVQVTGRRISATAEDGNKFAKLIVETDTFGSRVRIKGAESEKYICMNRGKLGKPSGKSKDCVFTEIVLENNYTAFQONARHEGWFMFAFTRQGRPRQASRSRQNOREAHFIKRLYQGQLPFPNHAEKQKQFEFVGSAPTRRTKRTRRPQPLT

Signal peptide:

amino acids 1-22

N-glycosylation site.

amino acids 9-13, 126-130

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 60-64

Casein kinase II phosphorylation site.

amino acids 65-69

Tyrosine kinase phosphorylation site.

amino acids 39-48, 89-97

N-myristoylation site.

amino acids 69-75, 188-194

Amidation site.

amino acids 58-62

HBGF/FGF family signature.

amino acids 103-128

FIGURE 12

ACTTGCCATCACCTGTTGCCAGTGTGGAAAAATTCTCCCTGTTGAATTTTGTGCACATGGAG
GACAGCAGCAAAGAGGGCAACACAGGCTGATAAGACCAGAGACAGCAGGGAGATTATTTTAC
CATACGCCCTCAGGACGTTCCCTCTAGCTGGAGTTCTGGACTTCAACAGAACCCCATCCAGT
CATTTTGATTGTGCTGTTTATTTTCTTTTCTTTTCCACCACATTGTATTTTAT
TTCCGTACTTCAGAAATGGGCCCTACAGACCACAAAGTGGCCAGCCATGGGGCTTTTTCCT
GAAGTCTTGGCTTATCATTTCCCTGGGGCTCTACTCACAGGTGTCCAAACTCCTGGCCTGCC
CTAGTGTGGTCGCGCTGCGACAGGAACCTTTGTCTACTGTAATGAGCGAAGCTTGACCTCAGTG
CCTCTTGGGATCCCGAGGGCGTAACCGTACTCTACCTCCACAACCAACAAATTAATAATGC
TGGATTTCCTGCAGAACTGCACAATGTACAGTCGGTGACACAGGTCTACCTGTATGGCAACC
AACTGGACGAATTCCTCATGAACCTTCCCAAGAAATGTGAGAGTTCTCCATTTGCAGGAAAAAC
AATATTTCAGACCATTTACGGGCTGCTCTTGCCAGCTCTTGAAGCTTGAAGAGCTGCACCT
GGATGACAACCTCATATCCACAGTGGGGGTGGAAGACGGGGCTTCCGGGAGGCTATTAGCC
TCAAATTGTTGTTTTGTCTAAGAATCACCTGAGCAGTGTGCTGTTGGGCTTCTGTGGAC
TTGCAAGAGCTGAGAGTGGATGAAAAATCGAATTGCTGCATATCCGACATGGCCTTCCAGAA
TCTCAGAGCTTGGAGCGTCTTATTGTGGACGGGAACCTCCTGACCAACAAGGGTATCGCGC
AGGCGACCTTCAGCCATCTCAACAGCTCAAGGAATTTCAATTGTACGTAATTCCGCTGTCC
CACCTCCTCCCGATCTCCAGGTACGCATCTGATCAGGCTCTATTGTGACAGACAACAGAT
AAACCAATTCTTTGACAGCCTTCTCAAATCTGCGTAAGCTGGAACGGCTGGATATATCCA
ACAAACCACTGCGGATGCTGACTCAAGGGGTTTTTGATAATCTCTCCAACCTGAAGCAGCTC
ACTGCTCGGAATAACCTTGGTTTTGTGACTGCAGTATTAATGGGTACAGAAATGGCTCAA
ATATATCCCTTCATCTCTCAACGTGCGGGGTTTCATGTGCCAAGTCTGAAACAGTCCGGG
GGATGGCGCTCAGGGAAATTAATATGAATCTTTGTCTGTCCACCACGACCCCGGCCTG
CCTCTCTCACCCAGCCCCAAGTACAGCTTCTCCGACCACTCAGCCTCCACCTCTCTAT
TCCAAACCTTAGCAGAAGCTACACGCTCCAACTCCTACCACTCGAAAATCTCCACGATTCT
CTGACTGGGATGGCAGAGAAAGAGTGACCCACCTATTTCTGAACGGATCCAGCTCTCTATC
CATTTGTGAATGATACTTCCATTCAAGTCAGCTGGCTCTCTCTCTTACCGTGATGGCATA
CAAACTCACATGGGTGAAAATGGGCCACAGTTTAGTAGGGGGCATCGTTCAGGAGCGCATAG
TCAGCGGTGAGAAGCAACACCTGAGCCTGGTTAACTTAGAGCCCCGATCCACCTATCGGATT
TGTTTAGTGCCACTGGATGCTTTTAACTACCGCGCGGTAGAAGACACCATTTGTTTCAAGGCG
CACCCACCATGCCTCCTATCTGAACAACGGCAGCAACACAGCGTCCAGCCATGAGCAGACGA
CGTCCCACAGCATGGGCTCCCCCTTTCTGCTGGCGGGCTTGATCGGGGGCGCGGTGATATTT
GTGCTGGTGGTCTTGCTCAGCGTCTTTGCTGGCATATGCACAAAAGGGCGCTACACCTC
CCAGAAGTGGAAATACAACGGGGCGCGCGAAAGATGATTATTGCGAGGCGAGGCACCAAGA
AGGACCACTCCATCTGGAGATGACAGAAACAGTTTTCAGATCGTCTCTTAAATAACGAT
CAACTCCTTTAAGGAGATTTTCAGACTGCAGCCCATTTACACCCCAATGGGGGCATTAAATTA
CACAGAGTGCCATATCCCCAACACATGCGATAGTGCACACAGCAGCGTGCCAGACCTGGAGC
ACTGCCATACGTCGACCGCAGAGGCCAGCGTTATCAAGGCGGACTTATAGACTCTTGAGAA
CACACTCGTGTGTGCACATAAAGACACGCAGATTACATTTGATAAATGTACACAGATGCAT
TTGTGCATTTGAATACTCTGTAATTTATACGGTGTACTATATAATGGGATTTAAAAAAGTG
CTATCTTTCTATTTCAGTTAATTACAAACAGTTTGTAACTCTTGTCTTTTAAATCTT

FIGURE 13

MGLQTTKWPSHGAFFLKSWLIISLGLYSQVSKLLACPSVCRNDFVYCNERSLTSVPLGIP
EGVTVLYLHNNQINNAAGFP AELHNQSVHTVYLYGNQLDEFFPMNL PKNVRVLHLQENNIQTI
SRAALAQLLKLEELHLDNDSISTVGVEDGAFREAI SLKLLPLSKNHLSSVPVGLPVDLQELR
VDENRIAVISDMAFQNLTSLERLIVDGNLLTNKGIAEGTFSHLTKLKEFSIVRNSLSHPPPD
LPGTHLIRLYLQDNQINHIPLTAFSNLRKLERLDISNNQLRMLTQGVDNLSNLKQLTARNN
PWFCDCSIKWVTEWLKYIPSSLNVRGFMCCQGPEQVRGMARELNMNLLSCPTTTPGLPLFTP
APSTASPTTQPPTL SIPNPSRSYTPPTPTTSKLPTIPDWDGREVRTPPISERIQLSIHVND
TSIQVSWLSLFTVMAYKL TWVKMGHSLVGGIVQERIVSGEKQHLSLVNLEPRSTYRICLVPL
DAFNRAVEDTICSEATTHASYLNNGSNTASSHEQTTSHSMGSPFLLAGLIGGAVIFVLVVL
LSVFCWHMHKKGRYTSQKWYNRGRRKDDYCEAGTKKDNSILEMTETSPQIVSLNNDQLLKG
DFRLQPIYTPNGGINYTDCHIPNNMRYCNSSVPDLEHCHT

Signal peptide:

amino acids 1-42

Transmembrane domain:

amino acids 542-561

N-glycosylation site.

amino acids 202-206, 298-302, 433-437, 521-525, 635-639, 649-653

Casein kinase II phosphorylation site.

amino acids 204-208, 407-411, 527-531, 593-597, 598-602, 651-655

Tyrosine kinase phosphorylation site.

amino acids 319-328

N-myristoylation site.

amino acids 2-8, 60-66, 149-155, 213-219, 220-226, 294-300,
522-528, 545-551, 633-639

Amidation site.

amino acids 581-585

Leucine zipper pattern.

amino acids 164-186

Phospholipase A2 aspartic acid active site.

amino acids 39-50

FIGURE 14

ACTTGGAGCAAGCGGCGGCGGCGGAGACAGAGGCGAGAGGCAGAAAGCTCGGTCTCGCTCCACGAGCG
ATCCCCGAGGAGAGCCGCGGCCCTTCGGCGAGGCGAAGAGCGGACGAGGAGAACCCGGGTGGCTGCGCCCCGCG
TCGCTTCCAGAGCGCGCGCGCTCGAGCCTTGCCCTCTTGCTGCGCTTGAAAT**TGG**AAAAGATGCTCGCAGGCT
GCTTCTGCTGATCTTCGACAGATCGTCTCTCCCTGCGAGGCCAGGGAGCGGTCACTCGGGAGGTCCATCT
CTAGGGGACAGACCGCTCGGACCCCAAGCCCGCAGACGGCCCTTCTGGAGAGTTCCTGTGAGAACAAAGCGGCGAGACC
TGCTTTTCATCATTTGACAGCTCTCGCAGGTGTCAACACCCATGACTATGCAAAAGGTCAAGGAGTTTCACTGTGGACA
TCTTGCAATTCTTGACATTTGGTCTCGATGTCAACCGAGTGGCGCTGCTCCAATATGGCAGCACTGTCAAGAAATG
AGTTTCTCCCTCAAGACCTTCAAGAGGAAGTCCGAGGTTGGAGCGTGCTGTCAAGAGGATGCGGCATCTGTCCACGG
GCACCATGACTGGGTCTGGCCATCCAGTATGCTTGAACATCGCATTTCTCAGAAGCAGAGGGGGCGGCGCCCTGA
GGAGAAATGTGCCACGGGTCTAATATGATCGTGACAGATGGGAGACCTCAGGACTCCGCTGGCGGAGGTGGCTGCTA
AGGCAAGGACAGGGCATCTAATCTTTGCCATTGGTGTGGGCCAGGTAGACTTCAACACCTTTGAAGTTCATTG
GGAGTGAGCCCCATGAGGACCATGTCTCTTGTGGCCAAATTTCAAGCCAGATTGAGACGCTGACCTCCGTGTPTCC
AGAAGAAAGTTGTGACCGGCCACATGTGACAGCACCTGGAGCATAAAGTGGCCCACTTCTGCATCAACATCCCTG
GCTCATAGCTGTGACAGGTGCAAAACAGGCTACATTTCAACTCGGATCAGACGACTTGCAGAAATCCAGGATCTGT
GTGCCATGGAGGCCAACACTGTGACAGCTCTGTGTGAATGTGCGGGCTCCTTCGTCTGCCAGTGCTACAGTG
GCTACGCCCCGTGGTGAAGGATGGGAAGAGGTGTGTGGCTGTGGACTACTGTGCTCAGAAAACCCAGGATGTGAAC
ATGAGTGTGTAATGTGATGGCTCTTACTCTTGGCCAGTGCCATGAAGGATTTGGCTTTAAACCCAGATGAAAAA
CGTGCAACAAGGATCAACTACTGTGCACTGAAACAAACCGGGCTGTGAGCATGAGTGCCTCAACATGGAGGAGAGCT
ACTACTGCGCTGCCACCGTGGCTACACTCTGGACCCCAATGGCAAACTCGCAGCCGAGTGGACCACTGTGCACT
AGCAGGACCATGCTGTGAGCAGCTGTGTCTGAAACCGGAGGATTCCTTCGTCTGCCAGTGCTCAGAAAGGCTTCC
TCACTCAACGAGGACCTCAAGACCTGTCTCCGGGTGGATTAATGCTGCTGTGAGTGACCATGGTTGTGAATACTCTCT
GTGTCAACATGGACAGATCTTTTGCTGTGAGTGTCTGAGGACACGCTGCTCCGACGCGATGGGAAGACGCTGTG
CAAAATTTGGACTCTTGTGCTCTGGGGGACCAAGGTTGTGAACATTCGTGTGTGAAGCAGTGAAGATTGGTTGTGT
GCCAGTGTCTTGAAGCTTATATGCTCCGTGAAGATGGAAAACTTGCAGAGGAAAGATGTCTGCCAAGCTATAG
ACCATGTGTGAAACCATTTTGTGTGAACAGTGAACGACTCATACGCTGCGAGTGTCTGGAGGGATTCCGGCTCG
CTGAGGATGGGAAACCTCTGCCAAGGAAGGATGTCTGCAAACTCAACCCACCATGGCTGCGAACACATTTTGTGTTA
ATAATGGGAATTCCTACATCTGCAATGTCTCAGAGGATTTGTTCTAGCTGAGGACGAAGGCGGCTGAGTGGGCTGCTCCAGT
GCCTGAAGGCCCAATGTGACCTGTCTTGTGATCGATGGATCAAAGATCTTGCAGAGAGAGATTTTGGAGTGT
TGAAGCAGTTTGTCACTTGAATATAGATTTCTTGACAAATTTCCCAAGCCGCTGAGTGGGGCTGCTCCAGT
ATTCTCACACAGGTCACACAGAGTTCACTCTGAGAACTTCAACTCAGCCAAAGACATGAAAAGCCGTGGGCC
ACATGAATACATGAGAGATGGCTCTATGACTGGGCTGGCCCTGAAACATGTTTGAGAGAGATTTTACCCAAAG
CAGAGGGGCCAGGCCCTTTTCCAAAGGCTGCCAGACAGCCATTTGTGTTACCGACGAGCGGGCTCAGAGT
ACGTCTCCGAGTGGGCGAGTAAAGCCAAAGCCCAATGGTATCACTATGTGCTGTGTGAGAGAGATTTTACCCAAAG
AGGAGGAACCTCAGAGAGATGGCTCTGAGCCCAACAAACAGCATCTCTTCTATGCCGAAGACTTCAGCAACATGG
ATGAGATAAGTGAAAACCTCAGAAAGGCACTGTGTAAGCTCTAGAAGACTCCGATCAATGCAAAATGTGAAAAACCTTATATGT
CAGGGGAACCTGCCAAAACCGTCCAAACAGCCAAACAGAACTGAGCCAGTCAACATAAATATCCAGACCTACTTT
CCTGTCTTAATTTTGCAGTGCACACAGATATCTGTTTGAAGAAGACAATCTTTTACGCTCTACACAAAAGCTTT
CCCATTCACAAAAACCTTCAGGAAGCCCTTTGGAGAAAAACACAGATCAATGCAAAATGTGAAAAACCTTATATGT
TCCAGAACCTTGCACAAACGAAGATGAAGAAAATTAACACAGCGCTTAGAAGAAATGACACAGAGAAATGGAAGCCC
TGGAAAACTCGCTGAGATACAGATGAAGATTAGAAAATCGCGACACATTTGTAGTCATTGTATCACGGATTACAAT
GAACGCAGTGCAGAGCCCCAAGCTCAGGCTATTTGTTAAATCAATAATGTTGTGAAGTAAAAACATCAGTACTGA
GAAACCTGTTTGGCAACAGAACAGAGAAAGTATACACTAACTTGTTAAATTTATCTAGGAAAAAATCTCT
TCAGAAATCTCAAGATGAATTTACAGGTGAGAAATGAATAAGTATGCAAGGTATTTTGTAAATATCTGTGGACAC
AACTGCTCTGTGCTCATCTTCGCTTAGTGTGCAATCTCATTTGACTTGAATTTGACATAAGTTTGGACAGGTCTTACTT
CTGTAGAACACTGCGCATAGGAATCTGCTTTTTTGTACTGCACTTACCTTGTATATATGATATGGATGATGT
CATAAAAATCATAGGACATAGTACTTGTGGAAACAGTTGGATTTTATCAATATTAATAATCCACACTCAG

0900572 071001

FIGURE 15

MEKMLAGCFLLILGQIVLLPAEARERSRGRSISRGRHARTHPOQTALLESSCENKRADLVFI I
DSSRSVNTHDYAKVKEFIVDILQFLDIGPDVTRVGLLQYGSTVKNESLKTFRKKESEVERAV
KRMRLHSTGTMGLAIQYALNIAFSEAEGARPLRENVPRVIMIVTDGRPDQDSVAEVAAKARD
TGILIFAIGVGQVDFNTLKSIGSEPHEDHVFLVANFSQIETLTSTVFQKKLCTAHMCSTLEHN
CAHFCINIPGSSVYCRCKQGYILNSDQTTCRIQDLCAMEDHNCEQLCVNVPGSFVCCQYSGYA
LAEDGKRCVAVDYCASENHGCEHECVNADGSYLCQCHEGFALNPDEKTCRINRYCALNKPGC
EHECVNMEESSYYCRCHRGYTLDPNGKTC SRVDHCAQQDHGCEQLCLNTEDSFVCQCSGFLI
NEDLKTC SRVDYCLLDHGC EYSCVNMDRSFACQCPEGHVLRSDGKTC AKLDS CALGDHGC E
HSCVSSSEDSFVCQCFEGYILREDGKTCRRKDVQCAIDHGC EHI CVNNSDDSYTCECLEGFRLA
EDGKRCRRKDVCKSTHHGCEHI CVNNGNSYICKCSEGFVLAEDGRRCKKCTEGPIDLVFVID
GSKSLGEENFEVVKQFVTGII DSLTISPKAARVGLLQYSTQVHTEFTLRNPNFSAKDMKKAVA
HMKYMGKGSMTGLALKHMFERSFTQGEGARPLSTRVPRAAIVFTDGRAQDDVSEWASKAKAN
GITMYAVGVGKAIEEBELQEIASEPTNKHLYAEDFSTMDIESEKLKKGICEALEDS DGRQDS
PAGELPKTVQQPTESEPVTTINI QDLLSCSNFAVQHRYLFEEDNLLRSTQKLSHSTKPSGSPL
EEKHDQCKCENLIMFQNLANEEVRKLTQRLEEMTQRMEALENRLRYR

Signal peptide:

amino acids 1-23

N-glycosylation site.

amino acids 221-225

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 115-119, 606-610, 892-896

Casein kinase II phosphorylation site.

amino acids 49-53, 118-122, 149-153, 176-180, 223-227, 243-247,
401-405, 442-446, 501-505, 624-628, 673-677, 706-710, 780-784,
781-785, 819-823, 866-870

N-myristoylation site.

amino acids 133-139, 258-264, 299-305, 340-346, 453-459, 494-500,
639-645, 690-696, 752-758, 792-798

Amidation site.

amino acids 314-318, 560-564, 601-605

Aspartic acid and asparagine hydroxylation site.

amino acids 253-265, 294-306, 335-347, 376-388, 417-423, 458-464,
540-546, 581-587

[illegible]

GGAGCGCCCTGGGTGTGACGGCTCGGCTCCCGCGCACGCTCCGGCCGTGCGCGAGCCTCG
 GCACCTGCAGGTCCGTGCGTCCCGCGGCTGGCGCCCCTGACTCCGTCCCGGCCAGGGAGGGC
CATGATTTCCCTCCCGGGGCCCTTGCTGACCAACTTGCTGCGGTTTTTGTTCCTGGGGCTGA
 GTGCCCTCGCGCCCCCTCGCGGGCCAGCTGCAACTGCACCTTGCCCGCCAACCGGTTGCGAG
 CGGTTGAGGGGAGGGGAAGTGGTGCTTCCAGCGTGGTACACCTTGACCGGGGAGGTGTCCTC
 ATCCAGCCATGGGAGGTGCCCTTTGTGATGTGGTCTTCAAACAGAAAAGAAAGGAGGATC
 AGGTGTTGTCTTACATCAATGGGGTCACAACAAGCAAACCTGGAGTATCCTTGGTCTACTCC
 ATGCCCTCCCGGAACCTGTCCCTGCGGCTGGAGGGTCTCCAGGAGAAAGACTCTGGCCCTTA
 CAGCTGCTCCGTGAATGTGCAAGACAAACAAGGCAAACTTAGGGGCCACAGCATCAAAACCT
 TAGAACTCAATGTACTGGTTCCTCCAGCTCCTCCATCCTGCCGTCTCCAGGGTGTGCCCAT
 GTGGGGGCAACGTGACCCCTGAGCTGCAGCTCTCCAAGGAGTAAGCCCGCTGTCCAATACCA
 GTGGGATCGGCAGCTTCCATCCTTCCAGACTTTCTTTGACACGACATATAGTGTCAATCGTG
 GGTCTTTAAGCCTCACCAACCTTTCCTCTTCCATGCGTGGAGTCTATGTTGCAAGGCCAC
 AATAGGTTGGGACATGCCAATGTAAATGTGACGCTGGAAGTGAGCACAGGGCCTGGAGCTGC
 AGTGGTTGCTGGAGCTGTTGTGGGTACCTGGTTGGACTGGGGTTGCTGGCTGGGCTGGTCC
 TCTTGTAACACCGCCGGGGCAAGGCCCTGGAGGAGCCAGCCAATGATATCAAGGAGGATGCC
 ATTGCTCCCGGACCTGCGCTGGCCCAAGAGCTCAGACACAATCTCCAAGAATGGGACCCT
 TTCTCTGTCACTCCGACAGAGCCTCCGGCCACCCCATGGCCCTCCAGGCCCTGGTGCAT
 TGACCCCCACGCCAGTCTCTCCAGCCAGGCCCTGCCCTACCAAGACTGCCACGACAGAT
 GGGGCCACCCTCAACCAATATCCCCATCCCTGGTGGGGTTTCTTCTCTGGCTTGAGCCG
 CATGGGTGCTGTGCTGTGATGGTGCCTGCCAGAGTCAAGCTGGCTCTCTGTGTATGATGAC
 CCCACCACCTATTGGCTAAAGGATTGGGGTCTCTCCTTCTATAAGGGTCACCTCTAGCAC
 AGAGGCCTGAGTCATGGGAAAGAGTCACTCCTGACCCCTTAGTACTCTGCCCCACCTCTC
 TTTACTGTGGGAAACCATCTCAGTAAGACCTAAGTGTCAGGAGACAGAAGGAGAAGAGGA
 AGTGGATCTGGAATTGGGAGGAGCCTCCACCCACCCCTGACTCCTCCTTATGAAGCCAGCTG
 CTGAAATTAGCTACTACCAAGAGTGAGGGGCAGAGACTTCCAGTCACTGAGTCTCCAGGC
 CCCCTTGATCTGTACCCACCCCTATCTAACACCAACCCTTGGCTCCCACTCCAGCTCCCTGT
 ATTGATATAACCTGTCAAGCTGGCTTGGTTAGGTTTTACTGGGGCAGAGGATAGGGAATCTC
 TTGATTAACCACTAACATGAAATATGTGTTGTTTTTCATTTCGAAATTTAAATTAAAGATACATAA
 TGTTTGTATGAAAAA

FIGURE 17

MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHL PANRLQAVEGGEVVLP AWYTLHG EVSS
SQPWEVPFVMWFFKQKEKEDQVLSYINGVTT SKPGVSLVYSMP SRNLSLRLEGLQE KDSGPY
SCSVNVQDKQGKSRGHSIKTLELNVLVPPAPP SCRLQGVPHVGANVTLSCQS PRSKPAVQYQ
WDRQLPSFQTFPAPALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLEVSTGPGAA
VVAGAVVGTTLVGLGLLAGLVLLYHRRGKALEEPANDIKEDAIAPRTL PWP KSSDTISKNGTL
SSVTSARALRP PHGPPRP GALTPTPSLSSQALPSR LPTTDGAHPQPI SP I PGGVSSSGLSR
MGAVPVMVPAQSQAGSLV

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 245-267

N-glycosylation site.

amino acids 108-112, 169-173, 213-217, 236-240, 307-311

N-myristoylation site.

amino acids 90-96, 167-173, 220-226, 231-237, 252-258, 256-262,
262-268, 308-314, 363-369, 364-370

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 164-175

FIGURE 18

CGCCACCACTGCGGCCACCGCCCAATGAAACGCCTCCCGCTCCTAGTGGTTTTTTCCACTTTG
TTGAATTGTTCTTACTCAAAATTGCACCAAGACACCTTTGTCTCCCAAAATGC AAAATGTGA
AATACGCAATGGAATTGAAGCTGCTATTGCAACATGGGATTTTCAGGAAATGGTGTCACAA
TTTGTGAAGATGATAATGAATGTGGAATTTAACTCAGTCCTGTGGCGAAAAATGCTAATTGC
ACTAACACAGAAAGGAAGTTATTATGTATGTGTGTACCTGGCTTCAGATCCAGCAGTAACCA
AGCAGGTTTATCACTAATGATGGAACCGTCTGTATAGAAAATGTGAATGCAAACTGCCATT
TAGATAAATGTCGTATAGCTGCAAAATATTAATAAACTTTAACAAAAATCAGATCCATAAAA
GAACCTGTGGCTTTGCTACAAGAAGTCTATAGAAATTCGTGACGATCTTTTACCAACAGATA
TATAAATTACATATAGAAAATATTAGCTGAATCATCTTCATTACTAGGTTACAAGAACAACA
CTATCTCAGCCAAGGACACCTTTCTAACTCAACTCTTACTGAAATTTGTAAAAACCGTGAAT
AATTTTGTTCAAAGGGATACATTTGTAGTTTGGGACAAGTTATCTGTGAATCATAGGAGAAC
ACATCTTACAAAACCTCATGCACACTGTTGAACAAGCTACTTTAAGGATATCCAGAGCTTCC
AAAAGACCACAGAGTTTGATACAAAATCAACGGATATAGCTCTCAAAGTTTTCTTTTTTGAT
TCATATAACATGAACATATTCATCTCATATGAATATGGATGGAGACTACATAAAATATATT
TCCAAAGAGAAAAGCTGCATATGATTCAAATGGCAATGTTGCAATTGCAATTTTATATTTATA
AGAGTATTGGTCCTTTGCTTTCATCATCTGACAACTTCTTATTGAAACCTCAAATATTATGAT
AATTTCTGAAGAGGAGGAAAAGAGTCATATCTTCAGTAATTTCACTCTCAATGAGCTCAAACCC
ACCCACATTTATATGAATCTGAAAAAATAACATTTACATTAAGTCATCGAAAGGTCACAGATA
GGTATAGAGCTATTGTGCACTTTTGGAAATTACTCACTGATACCATGAATGGCAGCTGGTCT
TCAGAGGGCTGTGAGCTGACATACCTCAAATGAGACCCACCTCATGCCGCTGTAATCACCT
GACACATTTGCAATTTTGATGTCTCTGGTCCTTCCATTGGTATTAAGATTATAATATTC
TTACAAGGATCACTCACTAGGAAATAATATTTCAGTGATTGTCTTGCCATATGCATTTTT
ACCTTCTGGTTCTTCAGTGAATTTCAAAGCACCAGGACAACAATTCACAAAAATCTTTGCTG
TAGCCTAATTTCTTGCGAACTGTTTTTCTTGTGGGATCAATACAAAATCAATAAGCTCT
TCTGTTCAATCATTTGCCGAGCTGCTACACTACTTCTTTTTAGCTGCTTTTGCATGGATGTGC
ATTGAAGGCATACATCTCTATCTCATTGTTGTGGGTGTCATCTACAAACAGGGATTTTTGCA
CAAGAAATTTTATATCTTTGGCTATCTAAGCCAGCCGCTGGTAGTTGGATTTTCGGCAGC
TAGGATACAGATATTATGGCACAACCAAGTATGTTGGCTTAGCACCGAAAAACAATTTTAT
TGGAGTTTTATAGGACCAGCATGCCATATCATCTTGTGTAATCTTTGGCTTTTGGAGTCAT
CATATACAAAAGTTTTTCGTCACTGCAAGGGTTGAAACCGAAGTTAGTTGCTTTGAGAACA
TAAGGTCTTGTGCAAGAGGAGCCCTCGCTCTTCTGTTCTTCTCGGCACCACTGGATCTTT
GGGTTCTCCATGTTGTGCAAGCATCAGTGGTTACAGCTTACCTTTCAGACTCAGCAATGC
TTTCCAGGGGATGTTCAATTTTTTTATTCCTGTGTGTTTTATCTAGAAAGATTCAAGAAGAA
ATTACAGATTGTTCAAAAATGTCCCTGTTGTTTGGATGTTTAAGGTAAACATAGAGAATG
GTGATAATTACAACTGCACAAAAATAAAAAATTCBAAGCTGTGGATGACCAATGTTATAAAAA
TGACTCATCAATATATCAATATTAACTACTAGACAAAAAGTATTTTAAATCAGTTTTTCT
GTTTATGCTATAGGAATCTGAGATAAAGGTAAAAATATGATCATATGATATACATATGT
TTTTCTATGTGAAATAGTTCTGTCAAAAATAGTATTGCAGATATTGGAAGTAATTTGGTTT
CTCAGGAGTGATATCACTGACCCAAGGAAAGATTTCTTTCTAACACGAGAAGTATATGAA
TGCTGTGAGAAATGTTTGACATAAAATAAAGAAATGAAGAACACATTTTACCATTTTGTGAA
TTGTTCTGAACATTAATGTCCACTAAAACAACTTAGACTCTGTTTGCTAAATCTGTTTCTT
TTTCTAATATTTCTAAAAAAAAGGTTTACCTCCACAATTGAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 19

MKRLPLLVVFSTLLNCSYTNCTKTPCLPNAKCEIRNGIEACYCNMGFSGNGVTICEDDNEC
GNLTQSCGENANCTNTEGSYYCMCVPGFRSSSNQDRFITNDGTVCIENVNANCHLDNVCIAA
NINKTLTKIRSIKEPVALLQEVYRNSVTDLSPTDIIITYIEILAESSSLGYKNNTISAKDTL
SNSTLTTEFVKTVNNFVQORDTFVVWDKLSVNHRRTHLTKLMHTVEQATLRISQSFQKTTEFDT
NSTDIALKVFFFDSYNMKHIHPHMNDGDYINIFPKRKAAYDSNGNVAVAFLYYKSIGPLLS
SSDNFLLPQNYDNSEEEERVVISVISMSSNPPTLYELEKITFTLSHRKVTDYRSLCAF
WNYSPTDMNGSWSSGCELTYSNETHTSCRCNHLTHFAILMSSSGPSIGIKDYNILTRITQLG
IIISLICLAICIFTWFFSEIQSTRRTTIHKNLCCSLFLAELVLVGINNTNTNKLFCSEIIAGL
LHYFFLAFAWMCIIEGIIHLYLIVVGVYINKGFLHKNFYIFGYLSPAVVVGFSALGYRYYGT
TKVCWLSTENNFIWFSFIGPACLIILVNLLAFGVIIYKVFRHTAGLKPEVSCFENIRSCARGA
LALLFLLGTTWIFGVLHVHASVVVTAYLFTVSNAFQGMFIFLFLCVLSRKIQEEYYRLFKNV
PCCFGCLR

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 430-450, 465-486, 499-513, 535-549, 573-593, 619-636,
648-664

N-glycosylation site.

amino acids 15-19, 21-25, 64-68, 74-78, 127-131, 177-181,
188-192, 249-253, 381-385, 395-399

Glycosaminoglycan attachment site.

amino acids 49-53

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 360-364

Casein kinase II phosphorylation site.

amino acids 54-58, 68-72, 76-80, 94-98, 135-139, 150-154,
155-159, 161-165, 181-185, 190-194, 244-248, 310-314, 325-329,
346-350, 608-612

Tyrosine kinase phosphorylation site.

amino acids 36-44, 669-677, 670-678

N-myristoylation site.

amino acids 38-44, 50-56, 52-58, 80-86, 382-388, 388-394,
434-440, 480-486, 521-527

Aspartic acid and asparagine hydroxylation site.

amino acids 75-87

[illegible]

TGGAACCATATCCTCCCTCATATGAATATGGATGGAGACTACATAAAATATATTTCCAAAGNG
AAAAGCCGGCATATGGATTCAAATGGCAATGTTGCAAGTGCATTTTTATATTATAAGAGTAT
TGGTCCCTTTGCTTTCATCATCTGACAACTTCTTATTGAAACCTCAAAAATATGATAATCT
GAAGAGGAGGAAAGAGTCATATCTTCAGTAATTTCAAGTCTCAATGAGCTCAAACCCACCCAC
ATTATATGAACCTTGAAAAATAACATTTACATTAAAGTCATCGAAAGGTCACAGATAGGTATA
GGAGTCTATGTGGCATTTTGGAACTACTCACCTGATACCATGAATGGCAGCTGGTCTTCAGAG
GGCTGTGAGCTGACATACTCAAATGAGACCCACACCTCATGCCGTGTAATCACCTGACACA
TTTTGCAATTTTATGATGTCCTCTGGCTCTCCATTGGTATTAAAGATTATAATATCTTACAA
GGATCACTCAACTAGGAATAATTATTTCACTGATTTGTCTTGCCATATGCATTTTACCTTC
TGGTCTTCTCAGTGAATTTCAAGCACAGGA

FIGURE 21

GCTCCAGCCAAGAACCTCGGGGCCGCTGCGCGGTGGGAGGAGTTCCCGAAACCCGGCCG
 CTAAGCGAGGCCTCCTCCTCCCGCAGATCCGAACCGGCTGGGCGGGGTACCCCGGTGCGGA
 CAAGAAGCCGCGCCTGCCTGCCCGGGCCCGGGAGGGGGCTGGGGCTGGGGCCGGAGGCGG
 GGTGTGAGTGGGTGTGTGCGGGGGCGGAGGCTTGATGCAATCCCGATAAGAAATGCTCGGG
 TGTCTTGGGCACCTACCCGTGGGGCCCGTAAGCGCTACTATATAAGGCTGCCGGCCCGGAG
 CCGCGCGCCGTGAGAGCAGGAGCGCTGCGTCCAGGATCTAGGGCCACGACCATCCCAACCC
 GGCACTCACAGCCCCCGCAGGCGATCCCGGTGCGCGCCAGCCTCCCGCACCCCATCGCCGG
 AGCTGCGCCGAGAGCCCCAGGGAGGTGCCATGCGAGCGGGTGTGTGTGGTCCACGTATGG
 ATCTGGCCGGCCTCTGGCTGGCCGTGGCCGGGGCGCCCCCTGCGCTTCTCGGACGCGGGGCC
 CCACGTGCACTACGGCTGGGGCGACCCCATCCGCCGTGCGGCGACCTGTACACCTCCGGCCCCC
 ACGGGCTCTCCAGCTGCTTCTGCGCATCCGTGCCGACGGCGTCTGGACTGCGCGGGGGC
 CAGAGCGCGCACAGTTTGTGAGATCAAGGCAGTCTCTGCGGACCGTGGCCATCAAGGG
 CGTGACAGCGTGCGGTACCTCTGCATGGGCGCCGACGGCAAGATGCAGGGGCTGCTTCACT
 ACTCGGAGGAAGACTGTGCTTTCGAGGAGGAGATCCGCCAGATGGCTACAATGTGTACCGA
 TCCGAGAGCACCGCCTCCCGGTCTCCCTGAGCAGTGCCAAACAGCGGCAGCTGTACAAGAA
 CAGAGGCTTCTTCCACTCTCTCATTTCTGCCCATGCTGCCCATGGTCCAGAGGAGCCTG
 AGGACCTCAGGGGCCACTTGAATCTGACATGTTCTCTTCGCCCTGGAGACCGACAGCATG
 GACCATTGGGCTTGTACCGGACTGGAGGCCGTGAGGAGTCCAGCTTTGAGAAGTAACT
 GAGACCATGCCCCGGGCTCTTCACTGCTGCCAGGGGCTGTGGTACCTGCAGCGTGGGGGACG
 TGCTTCTACAAGAAGCTCTGAGTCCACGTTCTGTTTAGCTTTAGGAAGAAACATCTAGAA
 GTTGTACATATTCAGAGTTTTCCATTGGCAGTGCCAGTTTCTAGCCAATAGACTTGTCTGAT
 CATAACATTGTAAGCCTGTAGCTTGCCAGCTGCTGCTGGGCCCCCATTTCTGCTCCCTCGA
 GGTTGCTGGACAAGCTGCTGCACGTGTCTCAGTTCTGCTTGAATACCTCCATCGATGGGGAAC
 TCACCTTCTTTGGAAAAATTCTTATGTCAAGCTGAAATTCTCTAATTTTCTCATCACTTC
 CCCAGGAGCAGCCAGAAGACAGGCAGTAGTTTTAATTTAGGAACAGGTGATCCACTCTGTA
 AAACAGCAGGTAATTTCACTCAACCCCATGTGGGAATTGATCTATATCTCTACTTCCAGGG
 ACCATTTGCCCTTCCAAAATCCCTCCAGGCCAGAACTGACTGGAGCAGGCATGGCCCCACAG
 GCTTCAGGAGTAGGGGAAGCCTGGAGCCCCACTCCAGCCCTGGGACAACCTTGAAATTTCCC
 CTGAGGCCAGTTCTGTCACTGGATGCTGTCTGAGAATAACTGTGTCGCCGGTGTCACTGC
 TTCCATCTCCCAGCCCCACAGCCCTCTGCCACCTCACATGCCTCCCATGGATTGGGGCCT
 CCCAGGCCCCACCTTATGTCAACCTGCATTTCTGTTCAAAAATCAGGAAAAGAAAAGAT
 TTGAAGACCCCAAGTCTTGTCAAATAACTTGCTGTGTGGAAGCAGCGGGGGAAGACCTAGAAC
 CCTTTCGCCAGCACTTGGTTTTTCCAACATGATATTTATGAGTAATTTATTTTGATATGTACA
 TCTCTTATTTTCTTACATTATTTATGCCCCCAAATTTATATTTATGTATGTAAGTGAGGTTTG
 TTTTGTATATTAATGAGGTTTGTGTTTGT

0000572 074104

FIGURE 22

MRSGCVVHVWILAGLWLAVAGRPLAFSDAGPHVHYGWDPIRLRHLYTSGPHGLSSCFLRI
RADGVVDCARGQSAHSLLEIKAVALTVAIKGVHSVRYLCMGADGKMQGLLQYSEEDCAFEE
EIRPDGYNVYRSEKHRLPVSLSAKQRQLYKNRGFLPLSHFLPMLPMVPEEPEDLRGHLESD
MFSSPLETDSMDPFGLVTGLEAVRSPSF EK

Signal peptide:

amino acids 1-22

Casein kinase II phosphorylation site.

amino acids 78-82, 116-120, 190-194, 204-208

N-myristoylation site.

amino acids 15-21, 54-60, 66-72, 201-207

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 48-59

FIGURE 23

CCCAGAAGTTCAAGGGCCCCGGCCTCTGCGCTCTGCCGCCGGGACCCCTCGACCTCCTCA
GAGCAGCCGGCTGCCGCCCCGGGAAGATGCGCAGGAGGAGCGCCACCGCCTCTCTGCTG
CTGCTGCGCTACCTGGTGGTCGCCCTGGGCTATCATAAGGCCTATGGGTTTTCTGCCCCAAA
AGACCAACAAGTAGTCACAGCAGTAGAGTACCAAGAGGCTATTTTAGCCTGCAAAACCCCAA
AGAAGACTGTTTTCTCCAGATTAGAGTGGAAGAACTGGGTCGGAGTGTCTCCTTTGTCTAC
TATCAACAGACTCTTCAAGGTGATTTTAAAAATCGAGCTGAGATGATAGATTCAATATCCG
GATCAAAAATGTGACAAGAAGTGATGCGGGGAAATATCGTTGTGAAGT*FAGTGCCCCATCTG
AGCAAGGCCAAAACCTGGAAGAGGATACAGTCACTCTGGAAGTATTAGTGGCTCCAGCAGTT
CCATCATGTGAAGTACCCCTCTTCTGCTCTGAGTGGAACGTGGTAGAGCTACGATGTCAAGA
CAAAGAAGGGAATCCAGCTCCTGAATACACATGGTTTAAGGATGGCATCCGTTTGCTAGAAA
ATCCCAGACTTGGCTCCCAAAGCACCAACAGCTCATACACAATGAATACAAAACCTGGAAC
CTGCAATTTAATACTGTTTCCAAACTGGACACTGGAGAATATTCCTGTGAAGCCCGCAATTC
TGTTGGATATCGCAGGTGTCTTGGGAAACGAATGCAAGTAGATGATCTCAACATAAGTGGCA
TCATAGCAGCCGTAGTAGTTGTGGCCTTAGTGATTTCCGTTTGTGGCCTTGGTGTATGCTAT
GCTCAGAGGAAAGGCTACTTTTCAAAGAAACCTCCTTCCAGAAGAGTAATTCTTCATCTAA
AGCCACGACAATGAGTGAAAATGTGCAGTGGCTCACGCCTGTAATCCAGCACTTTGGAAGG
CCGCGCGCGGGCGGATCACGAGGTCAAGGAGTTCTAGACCAGTCTGGCCAATATGGTGAACCC
CATCTCTACTAAAAATACAAAAATTAGCTGGGCATGGTGGCATGTGCCTGCAGTTCAGCTGC
TTGGGAGACAGGAGAATCACTTGAACCCGGGAGGCGAGGTTGCAGTGAGCTGAGATCACGC
CACTGCAGTCCAGCCTGGGTAAACAGAGCAAGATTCATCTCAAAAAATAAAATAAATAAATA
AATAAATACTGGTTTTTACCTGTAGAATTCTTACAATAAATATAGCTTGATATTC

FIGURE 24

MARRSRHRLLLLLLRYLVVALGYHKAYGFSAPKDQQVVTAVEYQEAILACKTPKKTVSSRLE
WKKLGRSVSFVYYQQTLOGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQQNLEED
TVTLEVLVAPAVPSCCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLENPRLGQSQT
NSSYTMNTKTGTQLQFNTVSKLDTGEYSCEARN SVGYRRCPGKRMQVDDLNI SGI IAAVVVVA
LVISVCGLGVCAQRKGYFSKETSFQKSNSSSKATTMSENVQWLTPVIPALWKAAGGSRGQEF

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 130-144, 238-258

N-glycosylation site.

amino acids 98-102, 187-191, 236-240, 277-281

Casein kinase II phosphorylation site.

amino acids 39-43, 59-63, 100-104, 149-153, 205-209, 284-288

N-myristoylation site.

amino acids 182-188, 239-245, 255-261, 257-263, 305-311

Amidation site.

amino acids 226-230

FIGURE 25

GACATCGGAGGTGGGCTAGCACTGAAACTGCTTTTCAAGACGAGGAAGAGGAGGAGAAAGAG
AAAGAAGAGGAAGATGTTGGGCAACATTATTATTAACATGCTCCACAGCCCGGACCCCTGGGCAT
CATGCTGCTATTCTTGCAAAATACTGAAGAAGCATGGGATTTAAATATTTTACTTCTTAAATAA
ATGAATTACTCAATCTCCTATGACCATCTATACATACTCCACCTTCAAAAAGTACATCAATA
TTATATCATTAAGGAAATAGTAACCTTCTCTTCTCCAATATGCATGACATTTTGGACAATG
CAATTGTGGCACTGGCACTTATTTTCAGTGAAGAAAACTTTGTGGTCTTATGGCATTTCATCA
TTTGACAATGCAAGCATCTTCTTATCAATCAGCTCCTATTGAACTTACTAGCACTGACTG
TGGAACTCCTTAAGGGCCCAATTACATTTCTGAAGAAGAAAGCTAAGATGAAGGCATGCCACT
CCGAATTCATGTGCTACTTGGCCTAGCTATCACTACACTAGTACAAGCTGTAGATAAAAAAG
TGGATTGTCCACGGTTATGTACGTTGAAATCAGGCCCTTGGTTTACACCCAGATCCATTAT
ATGGAAGCATCTACAGTGGATTGTAATGATTTAGGTCTTTTAACTTTCCAGCCAGATTGCG
AGCTAACACACAGATTTCTCTCTACAGACTAACATATTGCAAAAATTGAATACTCCACAG
ACTTTCAGTAAACCTTACTGGCCTGGATTATCTCAAAACAATTTATCTTCAGTCCCAAT
ATTAATGTAAAAAAGATGCCCTCAGCTCCTTCTGTGTACCTAGAGGAAAAACAACCTTACTGA
ACTGCTTCAAAAAATGTCTGTCCGAAGTGAAGCACTTACAAGAACTCTATATTAATCACAACT
TGCTTTCTACAATTTCACTTGGAGCCTTATTGGCCTACATAATCTTCTTCAGCTTCACTC
AATTCAAATAGATTGCAGATGATCAAAGTAAAGTGGTTTGATGCTCTTCCAATCTAGAGAT
TCTGATGATTGGGAAAAATCCAATTATCAGAATCAAAGACATGAACCTTAAAGCCTCTTATCA
ATCTTCGAGCCTGGTTATAGCTGGTATAAACCTCACAGAAATACCAGATAACGCGTTGGTT
GGACTGGAAGAACTTAGAAGCATCTCTTTTACGATAACAGGCTTATTAAAGTACCCCATGT
TGCTCTTCAAAAGTTGTAATCTCAAATTTTGGATCTAAATAAAAACTCCTATTAATAGAA
TACGAAGGGGTGATTTTAGCAATATGCTACACTTAAAGAGTTGGGGATAAAATAATATGCCCT
GAGCTGATTTCCATCGATAGTCTTGTCTGGGATAACCTGCCAGATTTAAGAAAAATAGAAGC
TACTAACCAACCTAGATTGTCTTACATTCAACCCCAATGCAATTTTCAGACTCCCCAAGCTGG
AATCACTCATGTGAACAGCAATGCTCTCAGTGCCCTGTACCATGGTACCATTTGAGTCTCTG
CCAAACCTCAAGGAAATCAGCATACACAGTAACCCCATCAGGTGTGACTGTGTCTATCCGTTG
GATGAACATGAACAAAACCAACATTCGATTCTAGGAGCCAGATTCACTGTTTTGCGTGGACC
CACCTGAATTCGAAGGTGAGAATGTTCCGCAAGTGCATTTTCAGGGACATGATGGAAATTTGT
CTCCCTCTTATAGCTCCTGAGAGCTTTCCTTCTAATCTAAATGTAGAAGCTGGGAGCTATGT
TTCCTTTCACTGTAGAGCTACTGCAGAACCCACAGCCTGAAATCTACTGGATAACACCTTCTG
GTCAAAAACTCTTGCCATAATACCTGACAGACAAGTTCTATGTCCATTCTGAGGGAACACTA
GATATAAATGGCGTAACTCCCAAGAAGGGGTTTATATACTGTATAGCAACTAACCTAGT
TGGCGCTGACTTGAAGTCTGTATGATCAAAGTGGATGGATCTTTTCCACAAGATAACAATG
GCTCTTTGAATATTAATAAAGAGATATTCAGGCCAATTCAGTTTTGGTGTCTCTGGAAGCA
AGTTCTAAATTTCTCAAATCTAGTGTAAATGGACAGCCCTTGTCAAAGCTGAAAAATCTCA
TGCTGCGCAAGGTGCTCGAATACCATCTGATGTCAAGGTATATAATCTTACTCATCTGAATC
CATCACTGAGTATAAAATTTGTATTGATATTTCCACCATCTATCAGAAAAACAGAAAAAAA
TGTGTAAATGTCAACCCAAAGGTTTGCAACCTGATCAAAAAGAGTATGAAAAGAATAATAC
CACAACACTTATGGCCTGTCTTGGAGGCCCTTCTGGGGATTATGGTGTGATATGTCTTATCA
GCTGCCCTCTCCAGAAATGAACGTGATGGTGGACACAGCTATGTGAGGAATTAATCTACAG
AAACCAACCTTTGTCATTAGGTGAGCTTTATCCTCTCTGATAAATCTCTGGGAGCAGGAAA
AGAAAAAGTACATCACTGAAAGTAAAAGCAACTGTTATAGGTTTACCAACAAATATGTCTT
AAAAACCAACAGGAACCTACTCCAAAAATGAAC

FIGURE 26

MKDMPLRIHVLLGLAITTLVQAVDKKVDPCRLCTCEIRPWFTPRSIYMEASTVDCNDLGLLT
FPARLPANTQILLQLQTNNAKIEYSTDFPVNLTGLDLSQNNLSSVTNINVKKMPQLLSVYLE
ENKLTTELPEKCLSELNLQELYINHNLSTISPGAFIGLHNLRLHLNSNRQLMINSKWFDA
LPNLIELMIGENPIIRIKDMNFKPLINLRSLVIAGINLTEIPDNALVGLENLESISFYDNRL
IKVPHVALQKVVLNLFDLNKNPINRIIRGDFSNMLHLKELGINNMPELISIDSLAVDNLPD
LRKIEATNNPRLSYIHPNAFFRLPKLESMLNSNALSALYHGHTIESLPNLKEISIHSPNIRC
DCVIRWMNMNKTNIRFMEPDSLFCVDPPEFQGNVRQVHFRDMMEICLPLIAPESFPSNLNV
EAGSYVSFHCRTAEPOPEIYWITPSGQKLLPNTLTDKFVYVHSEGTLDINGVTPKEGGLYTC
IATNLVGADLKSVMIKVDGSFPQDNNGSLNIKIRDIQANSVLVSWKASSKILKSSSVKWTA
FVKTENSHAAQSARIPSDVKVYNLTHLNPSTYKICIDIPTIYQKNRKKCVNVTTKGLHPDQKE
YEKNNTTTLMACLGGLGIIGVICLISCLSPMNCDDGGHSYVRNYLQKPTFALGELYPPPLIN
LWEAGKEKSTSLKVKATVIGLPTNMS

Signal sequence:

amino acids 1-22

Transmembrane domain:

amino acids 633-650

N-glycosylation site.

amino acids 93-97, 103-107, 223-227, 382-386, 522-526, 579-583,
608-612, 624-628, 625-629

Casein kinase II phosphorylation site.

amino acids 51-55, 95-99, 242-246, 468-472, 487-491

Tyrosine kinase phosphorylation site.

amino acids 570-579

N-myristoylation site.

amino acids 13-19, 96-102, 158-164, 221-227, 352-358, 437-443,
491-497, 492-498, 634-640, 702-708

Cell attachment sequence.

amino acids 277-280

Year	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099
Age	0	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99

GCCCGGGAGCTGGCGCAAGGTGCCCAAGCAAGGAAAGAAATAATGAAGAGACACATGTGTTAG
 CTGCAAGCCTTTTGAAACACGCAAGAGGAAATCAATAGTGTGGACAGGGCTGGAACTTTAC
 CACGCTTGTTGGAGTAGATGAGGAATGGGCTCGTGATTATGCTGACATTCAGACATGAATCT
 GGTAGACCTGTGGTTAACCGTTCCTCTCCAATGCTGTCCTCCTACAAAGTTTTGTTCTTA
 TGATACTGTGCTTTCAATTCTGCCAGTATGTGTCCCAAGGGCTGTCTTTGTTCTTCCTCTGGG
 GGTTTAAATGTCACCTGTAGCAATGCAAATCTCAAGGAAATACCTAGAGATCTTCCTCCTGA
 AACAGTCTTACTGTATCTGGAGTCTCCAATCAGATCACATCTATTCCCAATGAAATTTTTAAG
 ACCTCCATCAACTGAGAGTCTCAACCTGCTCCAAAATGGCATTTGAGTTTATCGATGAGCAT
 GCTTCTCAAAGGAGTAGTGTAAACCTTGACATCTGCACTGTGCGACAATCGGATTCGAAAG
 TGTGCAACAAAATGCTTCAATAACTGAAGGCCAGGGCCAGAATTGCCAACACCCCTGGC
 ACTGCGACTGTACTCTACAGCAAGTCTGAGGAGCATGGCGTCCAATCATGAGACAGCCAC
 AACGTGATCTGTAAAAAGTCCGTGTTGGATGAACATGCTGGCAGACCATTCTCAATGCTGC
 CAACGACGCTGACCTTTGTAACTCCCTAAAAAACTACCGATTATGCCATGCTGGTCACCA
 TGTTTGGCTGGTTCACTATGGTGATCTCATATGTGGTATATTATGTGAGGCAAAATCAGGAG
 GATGCCCGGAGACACCTCGAATACTTGAAATCCCTGCCAAGCAGGCAGAGAAGAACGAGATGA
 ACCTGATGATATTAGCACTGTGGTATAGTGTCCAAACTGACTGTCAATTGAGAAAGAAAGAAA
 GTAGTTTGCgATTGCAGTAGAAATAAGTGGTTTACTTCTCCCATCCATTGTAACACATTTGAA
 ACTTTGTATTTCAAGTTTTTTTTTGAATTATGCCACTGCTGAACCTTTTGAACAAACACATCAACA
 TAAATAAATTGAGTTTAGGTGATGACACCCCTTAATTTGATCCCCGATGGTATATTCTGAGT
 AAGACTACTATTGCAACTATTAGTATGCATCTCACTATTTAATAATGAAATTTATTTTTTTT
 AATTTTAAAGCAAATAAAGCTTTAACTTTGAACCATGGGAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 28

MNLVDLWLTRSLSMCLLLQSFVLMILCFHSASMC PKGCLC SSSGGLNVTC SNANLKEIPRDL
PPETVLLYLD SNQITSIPNEIFKDLHQLRVLNLSKNGIEFIDEHAFKGV AETLQTLDSL DNR
IQSVHKNAFNNLKARARIANNPWHCDCTLQQVLRSMASNHETAHNVIC KTSVLDEHAGR PFL
NAANDADLCNL PKKTTDYAMLVTMFGWFTMVISYVVYYVRQNQEDARRHLEYL KSLPSRQKK
ADEPDDISTVV

Signal sequence:

amino acids 1-33

Transmembrane domain:

amino acids 205-220

N-glycosylation site.

amino acids 47-51, 94-98

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 199-203

Casein kinase II phosphorylation site.

amino acids 162-166, 175-179

N-myristoylation site.

amino acids 37-43, 45-51, 110-116

FIGURE 29

ACCGAGCCGAGCGACC GAAGCGCGCCCGAGATG CAGGTGAGCAAGAGGATGCTGGCGGGG
GGCGTGAGGAGCATGCCAGCCCCCTCCTGGCCTGCTGGCAGCCCATCCTCCTGCTGGTGTCT
GGGCTCAGTGCTGT CAGGCTCGGCCACGGGCTGCCCGCCCGCTGCGAGTGCTCCGCCCAGG
ACCGCGCTGTGCTGTGCCACCGCAAGTGCTTTGTGGCAGTCCCCGAGGGCATCCCCACCGAG
ACGCGCCTGCTGGACCTAGGCAAGAACCGCATCAAAACGCTCAACCAGGACGAGTTCCGCCAG
CTTCCCCGACCTGGAGGAGCTGGAGCTCAACGAGAACATCGTGAGCGCCGTGGAGCCCGCGG
CCTTCAACACACCTCTTCAACCTCCGGACGCTGGGTCTCCGAGCAACCCGCTGAAGCTCATC
CCGCTAGGCGCTCTTCACTGGCCTCAGCAACCTGACCAAGCAGGACATCAGCGAGAACAAAGAT
CGTTATCCTACTGGACTACATGTTTTCAGGACCTGTACAACCTCAAGTCACTGGAGGTTGGCG
ACAATGACCTCGTCTACATCTCTCACCGCGCCTTCAGCGGCTCAACAGCCTGGAGCAGCTG
ACGCTGGAGAAATGCAACCTGACCTCCATCCCCACGAGGCGCTGTCCACCTGCACGGCCT
CATCGTCTTGAGGCTCCGGCACCTCAACATCAATGCCATCCGGGACTACTCCTTCAAGAGGC
TGTACCGACTCAAGGTCTTGAGATCTCCCACTGGCCCTACTTGGACACCATGACACCCAAC
TGCCTCTACGGCCTCAACCTGACGTCCCCTGTCCATCACACACTGCAATCTGACCCGTGTGCC
CTACCTGGCCGTCGCCACCTAGTCTATCTCCGCTTCTCTCAACCTCTCTACAAACCCCATCA
GCACCATTTAGGGCTCCATGTTGCATGAGCTGCTCCGGCTGCAGGAGATCCAGCTGTTGGGC
GGGCAGCTGGCCGTGGTGGAGCCCTATGCTTTCGCGGCCCTCAACTACCTGCGCGTGCTCAA
TGTCTCTGGCAACAGCTGACCCACTGGAGGAATCAGTCTTCCACTCCGTGGGCAACCTGG
AGACACTCATCCTGGACTCCAACCGCTGGCCTGCGACTGTCCGGTCTGTGGGTGTTCGG
CGCCGCTGGCGCTCAACTTCAACCGGAGCAGCCCCAGTGCGCCACGCCCGAGTTTGTCCA
GGGCAAGGAGTTCAAGGACTTCCCTGATGTGCTACTGCCAACTACTTCACTGCCCGCCGG
CCCGCATCCGGACCGCAAGGCCAGCAGGTGTTGTGGACGAGGGCCACAGGTGCAGTTT
GTGTGCCGGCCGATGGCGACCCGCGCCCGCCCATCCTCTGGCTCTCACCCCGAAAGCACCT
GGTCTCAGCCAAAGAGCAATGGGCGGCTCACAGTCTTCCCTGATGGCACGCTGGAGGTGCGCT
ACGCCCAGGTACAGGACAACGGCACGTACCTGTGCATCGCGGCCAACCGCGGCGGCAACGAC
TCCATGCCCGCCACCTGTCATGTGCGCAGCTACTCGCCCGACTGGCCCCATCAGCCCCAACAA
GACCTTCGCTTTCATCTCCAACAGCCGGCGGAGAGGCAACAGCACCCGCGCCACTG
TGCCTTTCCTTCGACATCAAGACCTCATCATCGCCACCACCATGGGCTTCATCTCTTTC
CTGGGCGTGTCTCTTCTGCTGCTGCTGCTGTTTCTTGGAGCCGGGGCAAGGGCAACAC
AAAGCAACACATCGAGATCGAGTATGTGCCCGAAAGTCGAGCGCAGGCATCAGCTCCGCCG
ACGCCCGCCGCAAGTTCAACATGAAGATGATATGAGGCGGGGGCGGGGGCAGGGACCCCCG
GGCGGCGGGCAGGGGAAGGGCCTGCTGCCACCTGCTCACTCTCCAGTCTTCCACCTC
CTCCCTACCTTCTACACACGTTCTCTTCTCCCTCCCGCTCCGTCCCTGCTGCCCCCCG
CCAGCCCTCACCACTGCCCTCTTCTTACCAGGACCTCAGAAGCCAGACCTGGGACCCCCA
CCTACAGGGGCATTGACAGACTGGAGTTGAAAGCCGACGAACCGACACGCGGCAGAGTCA
ATAATTCAATAAAAAAGTTACGAACTTTCTCTGTAACCTGGGTTTCAATAATTATGGATTTT
TATGAAAACCTGAAATAATAAAAAGAGAAAAAACTAAAAAAAAAAAAAAAAAAAAA

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FIGURE 30

MQVSKRMLAGGVSRMSPSPLLACWQPIILLVLGSLVSGSATGCPPRCECSAQDRAVLCHRKCF
VAVPEGIPTETRLDLGKNRIKTLNQDEFASFPHLEELNENIVSAVEPGAFNNLFLNRLTL
GLRSNRLKLIPLGVFTGLSNLTKQDISENKIVILLDYMFDLYNLKSLEVGDNDLVYISHRA
FSGLNSLEQLTLEKCNLTISIPTALSHLHGLIVLRLRHININAI RDYSFKRLYRLKVLEISH
WPYLDTMTPNCLYGLNLTSLSITHCNLTAVPYLAVRHLVYLRLNLSYNPISTIEGSMHLHEL
LRLQEIQLVGGQLAVVEPYAFRGLNYLRVLNVSGNQLTITLEESVFSVGNLETILDSNPLA
CDCRLLWVFRRRWRNLNFRNQOPTCATPEFVQGKEFKDFPDVLLPNYFTCRRARIRDRKAQQV
FVDEGHTVQFVCRADGDPPIILWLSPRKHLVSAKSNGRLTVPFDGTLEVRYAQVQDNGTYL
CIAANAGGNDSPAHLHVRSYSPDWPHQPNKTFAFISNQPGEGEANSTRATVPFPFDIKTLI
IATTMGFISFLGVVFLCLVLLFLWSRGKGN TKHNIEIEYVPRKSDAGISSADAPRKFNMKMI

Signal sequence:

amino acids 1-41

Transmembrane domain:

amino acids 556-578

N-glycosylation site.

amino acids 144-148, 202-206, 264-268, 274-278, 293-297, 341-345,
492-496, 505-509, 526-530, 542-546

Casein kinase II phosphorylation site.

amino acids 49-53, 108-112, 146-150, 300-304, 348-352, 349-353,
607-611

Tyrosine kinase phosphorylation site.

amino acids 590-598

N-myristoylation site.

amino acids 10-16, 32-38, 37-43, 113-119, 125-131, 137-143,
262-268, 320-326, 344-350, 359-365, 493-499, 503-509, 605-611

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 32-43

FIGURE 31

CCCACGCGTCCGCACCTCGGCCCCGGGCTCCGAAGCGGCTCGGGGCGCCCTTTCGGTCAAC
ATCTAGTACCAACCCCTCCCATCCCCAGCCCCGGGATTACGGCTCGCCAGCGCCAGCC
AGGAGCCGCGCCGGGAAGCGCGATGGGGGCCCCAGCCGCCTCGTTCCTGCTCCTGCTCCTG
TGTTTCGCTGCTGCTGGGCGCCCCGGCGGGCCAACTCTCCAGGACGACAGCCAGCCCTGG
ACATCTGATGAAACAGTGGTGGCTGGTGGCACCGTGGTGTCTCAAGTGCCAAAGTGAAAGATCA
CGAGGACTCATCCCTGCAATGGTCTAACCTGCTCAGCAGACTCTCTACTTTGGGGAGAAGA
GAGCCCTTCGAGATAATCGAATTACAGCTGGTTACCTCTACGCCCCACGAGCTCAGCATCAGC
ATCAGCAATGTGGCCCTGGCAGACGAGGGCGAGTACACCTGCTCAATCTTCACTATGCCTGT
GCGAACTGCCAAGTCCCTCGTCACTGTGCTAGGAATTCACAGAAGCCCATCATCACTGGTT
ATAAATCTTCATTACGGGAAAAAGACACAGCCACCCCTAACTGTCACTCTCTGGGAGCAAG
CCTGCAGCCCGGCTCACCTGGAGAAAGGGTGACCAAGAACTCCACGGAGAACCAACCCGCAT
ACAGGAAGATCCCAATGGTAAACCTTCACTGTGACGAGCTCGGTGACATTCAGGTTACCC
GGGAGGATGATGGGGCGAGCATCGTGTGCTCTGTGAACCATGAATCTCTAAAGGGAGCTGAC
AGATCCACCTCTCAACGCATTGAAGTTTTATACACCAACTGCGATGATTAGGCCAGACCC
TCCCATCTCTGAGGGCCAGAAGCTGTTGCTACACTGTGAGGGTCGCGGCAATCCAGTCC
CCCAGCAGTACCTATGGGAGAAGGAGGGCAGTGTGCCACCCCTGAAGATGACCCAGGAGAGT
GCCCTGATCTTCCCTTTCTCAACAAGAGTGACAGTGGCACCTACGGCTGCACAGCCACCAG
CAACATGGGCAGCTACAAGGCCTACTACACCCCTCAATGTTAATGACCCAGTCCGGTGCCCT
CCTCCTCCAGCCTACCACGCCATCATCGGTGGGATCGTGGCTTTCATTGTCTTCTGCTG
CTCATCATGCTCATCTTCTTGGCCACTACTTGATCCGGCACAAAGGAACCTACCTGACACA
TGAGGCAAAAGGCTCCGACGATGCTCCAGACGCGGACACGGCCATCATCAATGCAGAAGGCG
GGCAGTCAGGAGGGGACGACAAGAAGGAATATTTATCTAGAGGCGCCTGCCCACTTCTCTGC
GCCCCCAGGGGCCCCTGTGGGGACTGTGTTGGGCGCTCACCAACCCGGACTTGTCACAGAGCAA
CCGAGGGCCGCCCCCTCCGCTTGCTCCCCAGCCACCCACCCCTGTACAGAATGTCTGC
TTTGGGTGCGGTTTTGTACTCGGTTTGAATGGGAGGGAGGAGGGCGGGGGAGGGGAGGG
TTGCCCTCAGCCCTTCCGTGGCTTCTCTGCATTGGGTTATTATTATTTGTAAACAATCC
CAAATCAAATCTGTCTCCAGGCTGGAGAGGCAGGAGCCCTGGGGTGAGAAAAGCAAAAACA
AACAAAAACA

FIGURE 32

MGAPAASLLLLLLFACCWAPGGANLSQDDSQPWTSDETVVAGGTVVLKCQVKDHEDSSLQW
SNPAQQTLYFGEKRALRDNRQLVTSTPHELSSISINVALADEGEYTCSTFTMPVRTAKSLV
TVLGIPQKPIITGYKSSLREKDTATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQEDPNGK
TFTVSSSVTFQVTREDDGASIVCSVNHESLKGADRSTSQRIEVLYTPTAMIRPDPPHPREGQ
KLLHCEGRGNPVPQQYLWEKEGSVPPPLKMTQESALIFPFLNKSDSGTYGCTATSNMGSYKA
YYTLNVNDPSPVPSSSSTYHAIIGGIVAFIVFLLLIMLIFLGHYLRHKGTYLTHEAKGSDD
APDADTAIINAEGGQSGGDDKKEYFI

Signal sequence:

amino acids 1-20

Transmembrane domain:

amino acids 331-352

N-glycosylation site.

amino acids 25-29, 290-294

Casein kinase II phosphorylation site.

amino acids 27-31, 35-39, 89-93, 141-145, 199-203, 388-392

N-myristoylation site.

amino acids 2-8, 23-29, 156-162, 218-224, 295-301, 298-304,
306-310, 334-340, 360-364, 385-389, 386-390

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

FIGURE 33

GGGGGTTAGGGGAGGAAGGAATCCACCCCAACCCCAAAACCCCTTTTCTTCTCCTTTCCTGG
CTTCGGACATTTGGAGCACTAAATGAACTTGAATTGTGTCTGTGGCGAGCAGGATGGTCCGCTG
TTACTTTGTGTGATGAGATCGGGGATGAATTGCTCGCTTTAAAAATGCTGCTTTGGATTCTGTT
GCTGGAGACGTCTCTTTGTTTTGCGCGCTGGAAACGTTACAGGGGACGTTTGCAAGAGAGA
TCTGTTCTGCAATTGAGATAGAAAGGGACCTACACGTAGACTGTGAAAAAAGGGCTTCACA
AGTCTGCGAGCTTTTCACTGCCCGGACTTCCAGTTTACCATTATTTCTGCATGGCAATTC
CCTCACTCGACTTTTCCCTAATGAGTTCGCTAACTTTTATAATGCGGTTAGTTTGCAATGG
AAAACAATGGCTTGCATGAAATCGTTTCCGGGGGCTTTTCTGGGGCTGCAGCTGGTGAAGAAGG
CTGCACATCAACAACAAGATCAAGTCTTTTCTGAAAGCAGACTTTTCTGGGGCTGGACGA
TCTGGAATATCTCCAGGCTGATTTTAATTTATTTACGAGATATAGACCCGGGGGCTTCCAGG
ACTTGAACAAGCTGGAGGTGCTCATTTTAAATGACAATCTCATCAGCACCCCTACCTGCCAAC
GTGTTCCAGTATGTGCCCATCACCCACCTCGACCTCCGGGGTAACAGGCTGAAAACGCTGCC
CTATGAGGAGGTCTTGGAGCAAAATCCCTGGTATTGCGGAGATCTGCTAGAGGATAAACCCTT
GGGACTGCACCTGTGATCTGCTCTCCCTGAAAGAATGGCTGGAACCAATTCCCAAGAATTGCC
CTGATCGGCCGAGTGGTCTGCGAAGCCCCACCAGACTCGAGGTTAAGAGCTCAATGAACAC
CACCGAACAGGACTTGTGTCTTTGAAAAACCGAGTGGATTCTAGTCTCCCGCGCCCCCTG
CCCAAGAAGAGACTTTTGCTCTTGGACCCCTGCCAACTCTTTTCAAGACAAATGGGCAAGAG
GATCATGCCACACAGGGTCTGCTCCAAACGGAGGTACAAAGATCCCAGGCAACTGGCAGAT
CAAAATCAGACCCACAGCAGCGATAGCGAGGTTAGCTCCAGGAACAAACCTTTAGCTAACCA
GTTTACCCTGCCCTGGGGCTGCAGCTGCGACCACATCCAGGGTGGGTTTAAAGATGAAC
TGCAACAACAGGAACGTGAGCAGCTTGGCTGATTTGAAGCCCAAGCTCTCTAACGTGACGA
GCTTTTCTACAGAGATAACAAGATCCACAGCATCCGAAAAATCGCACTTTGTGGATTACAAGA
ACCTCATTCTGTGGATCTGGGCAACAATAACATCGCTACTGTAGAGAACCAACACTTTCAAG
AACCTTTTGGACCTCAGGTGGCTATACATGGATAGCAATTACCTGGACACGCTGTCCCGGGA
GAAATTCGCGGGGCTGCAAAACCTAGAGTACCTGAACGTGGAGTACAACGCTATCCAGCTCA
TCCTCCCGGGCACTTTCAATGCCATGCCAAACTGAGGATCCTCATTCTCAACAACAACCTG
CTGAGGTCCCTGCCTGTGGAGCTGTTTCGCTGGGGTCTCGCTCTTAAACTCAGCCTGCACAA
CAATTACTTTCATGTACTCCCGGTGGCAGGGGTGCTGGACCAAGTTAACTCCATCATCCAGA
TAGACCTCCACGGAACCCCTGGGAGTGCTCTGCAACAATTGTCCTTTCAAGCAGTGGGCA
GAACGCTTGGGTTCCGAAGTGTGATGAGCGACCTCAAGTGTGAGACGCGGTTGAACCTTCTT
TAGAAAGGATTTTCATGCTCCTCTCCAATGACGAGATCTGCCCTCAGCTGTACGCTAGGATCT
CGCCACGTTAACTTCGCACAGTAAAAACAGCACTGGGTTGGCGGAGACCGGGACCACTCC
AACTCTACCTAGACACCAGCAGGGTGTCCATCTCGGTGTTGGTCCCGGACGTGCTGCTGGT
GTTTGTCACTCTCCGCTTACCCGTGGTGGGCATGCTCGTGTTTATCCTGAGGAACCGAAAGC
GGTCCAAGAGACGAGATGCCAACTCTCCGCGTCCGAGATTAATTCCTTACAGACAGTCTGT
GACTCTTCTACTGGCACAATGGGCCTTACAACGACAGATGGGGCCACAGAGTGTATGACTG
TGGCTCTCACTCGCTCTCAGACTAAGACCCCAACCCCAATAGGGAGGGCAGAGGGAAGCGG
ATACATCCTTCCCCACCGCAGGCACCCCGGGGCTGGAGGGGCGTGTATCCCAAAATCCCCGCG
CCATCAGCTGAGTGGGCATAAGTAGATAAATAACTGTGAGCTCGCACAAACCGAAAGGGCCT
GACCCTCTTGTAGTCTCCTCTTGAACAACAAGAGCAGACTGGGAGAGCTGGGAGAGCGTGA
GCCAGCTCGCTCTTTGCTGAGAGCCCTTTTGACAGAAAGCCGACACGACCTGTCTGGAAG
AACTGACAGTGCCTCGCCCTCGGCCCCGGGGCCTGTGGGGTGGATGCGCGGTTCTATAC
ATATATACATATATACATCTATATAGAGAGATAGATATCTATTTTCCCTGTGGATTAG
CCCCGTGATGGCTCCCTGTTGGCTACGAGGGATGGGCAGTTGCACGAAGGCATGAATGTAT
TGTAATAAGTAACCTTTGACTTCTGAC

FIGURE 35

AGTCGACTGCGTCCCCTGTACCCGGCGCCAGCTGTGTTCTGTACCCAGAACTCAAGGGC
TGCAACGGGCTGGCAGCGCTCCGCACACATTTCTGTGCGGGCTAAGGGAACTGTTGGC
CGCTGGGCCCGCGGGGGATTCTTGGCAGTTGGGGGTCGTGCGGAGCGAGGGCGGAGGG
AAGGGAGGGGGAACCGGTTGGGGAAGCCAGCTGTAGAGGGCGGTGACCGCGCTCCAGACAC
AGCTCTGCGTCTCGAGCGGGACAGATCCAAGTTGGGAGCAGCTCTGCGTGC GGGGCCTCAG
AGAATGAGGCGCGGCTTCGCCCTGTGCTCTCTGGCAGGCGCTCTGGCCGGGGCGGGCGG
CGCGGAACACCCCACTGCCGACCGTGTGGCTGCTCGGCCCTCGGGGCTCTAGCAGCTGCG
ACCACGCTACCATGAAGCGCGAGGCGGCGGAGGAGGCTGCAATCTGCGAGGTGGGGCGCTC
AGCACCGTGCCTGCGGGCGCCGAGCTGCGCGCTGTGCTCGCGCTCTGCGGGCAGGCCCAGG
GCCCGGAGGGGGCTCCAAAGACCTGTGTTCTGGGTGCGACTGGAGCGCAGGCGTTCCTCACT
GCACCTGGAGAACGAGCCTTTGCGGGGTTTCTCTGGCTGTCTCCGACCCCGCGGCTCTC
GAAAGCGACACGCTGCGAGTGGGTGGAGGAGCCCCAACGCTCTGCGACCGCGCGGAGATGCGC
GGTACTCCAGGCCACCGTGGGGTCGAGCCCGCAGGCTGGAAGGAGATGCGATGCCACCTGC
GCGCAACGGCTACCTGTGCAAGTACCAGTTTGAGGTCTTGTGTCTGCGCCGCGCCCGGG
GCCGCTCTAACTTGAGCTATCGCGCGCCCTTCAGCTGCACAGCGCGCTCTGGACTTCAG
TCCACTGGGACCGAGGTGAGTGCCTCTGCGGGGACAGCTCCCGATCTCAGTTACTTGCA
TCGCGGACGAAATCGGCGCTCGCTGGGACAACTCTCGGGCGATGTGTGTGTCTCCCTGCCCC
GGGAGGTACCTCCGTGCTGGCAATGCGCAGAGCTCCCTAACTGCCTAGACGACTTGGGAGG
CTTTGCGTGCGAATGTGCTACGGGCTTCGAGCTGGGGAAGGACGCGCTCTTGTGTGACCA
GTGGGGAAGGACAGCGACCCCTTGGGGGACCGGGGTGCCACCAAGGCGCCCGCGGCCACT
GCAACCGCCCGTGCCGAGAGAACATGGCCAATCAGGCTCGACGAGAAGCTGGGAGAGAC
ACCCTTTGTCTCCTGAACAAGACAATTCAGTAACATCTATTCTGAGATTCTCGATGGGGAT
CACAGAGCAGATGTCTACCTTCAAATGTCCCTTCAAGCCGAGTCAAAGGCCATATCACC
CCATCAGGGAGCGTGATTTCCAAGTTTAATTCTACGACTTCCTCTGCCACTCCTCAGGCTTT
CGACTCTCTCTGCGGTGGTCTTCATATTTGTGAGCACAGCAGTAGTAGTGTGGTGATCT
TGACCATGACAGTACTGGGGCTTGTCAAGCTCTGCTTTCACGAAAGCCCTCTTCCAGCCA
AGGAAGGAGTCTATGGGCCCGCGGGCTTGAGAGTGATCCTGAGCCCGCTGCTTTGGGCTC
CAGTTCTGCACATTGCACAAACAATGGGGTGAAAGTTCGGGACTGTGATCTGCGGGACAGAG
CAGAGGGTCTCTGTGCGGAGTCCCCTCTTGGCTCTAGTGATGCAATAGGAAACAGGGGA
CATGGGCACTCCTGTGAACAGTTTTTCACTTTTGTATGAAACGGGGAAACCAAGAGGAACCTAC
TTGTGTAACGACAATTTCTGCAGAAATCCCCCTTCTCTAAATTCCTTTACTCCAAGTACG
GAGCTAAATCAGAACTGCACTCCTTCCCTGATGATAGAGGAAGTGAAGTGCCCTTAGGA
TGGTGATACTGGGGACCGGGTAGTGCTGGGGAGAGATATTTCTTATGTTTATTCGAGAA
TTTGAGAAAGTATTGAACCTTTTCAAGCATTTGGAACAAATAGAACACAATATAATTACCA
TTAAAAATAATTTTCAACAAATGGAAGGAAATGTTCTATGTGTTTCAAGCTAGGAGTAT
ATTGTTTCGAAATCCAGGGAAAAAATAAAAAATAAAAAATTAAGGATTGTTGAT

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FIGURE 36

MRPAFALCLLWQALWPGPGGGEHPTADRAGCSASGACYSLHHATMKRQAAEEACILRGGALS
TVRAGAEI RAVLALLRAGPGPGGSKDLLFWVALERRRSHCTLENEPLRGFSWLSSDPGGLE
SDTLQWVEEPQRSCTARRCAVLQATGGVEPAGWKEMRCHLRANGYLCKYQFEVLC PAPRPGA
ASNL SYRAPFQLHSAALDFSPPGTEVSALCRGQLPISVTCIADEIGARWDKLSGDVLCPCPG
RYLRAGKCAELPNCDDLGGFACATGFELGKDGRSCVTSGEQQPTLGGTGVPTRRPPATA
TSPVPQRTWPIRVDEKLGETPLVPEQDNSVTSIPEIPRWGSQSTMSTLQMSLQAESKATITP
SGSVISKFNSTTSSATPQAFDSSSAVVFI FVSTAVVVLVILTMIVLGLVKLCFHESPPSSQPR
KESMGPPGLESDPEPAALGSSSAHCTNNGVKVGDCDLRDRAEGALLAESPLGSSDA

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 399-418

N-glycosylation site.

amino acids 189-193, 381-385

Glycosaminoglycan attachment site.

amino acids 289-293

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 98-102, 434-438

Casein kinase II phosphorylation site.

amino acids 275-279, 288-292, 342-346, 445-449

N-myristoylation site.

amino acids 30-36, 35-41, 58-64, 59-65, 121-127, 151-157,
185-191, 209-215, 267-273, 350-356, 374-380, 453-459, 463-469,
477-483

Aspartic acid and asparagine hydroxylation site.

amino acids 262-274

FIGURE 37

CGGACGCGTGGGATTTCAGCAGTGGCCTGTGGCTGCCAGAGCAGCTCCTCAGGGGAAACTAAG
CGTCGAGTCAGACGGCACCATAATCGCCTTTAAAGTGCCTCCGCCCTGCCGGCCGCGTATC
CCCCGGCTACTGGGCCCGCCCCGGCGGTGCGCGGTGAGAGGGAGCGCGCGGGCAGCCGA
GCGCCGGTGTGAGCCAGCGCTGCTGCCAGTGTGAGCGCGGTGTGAGCGCGGTGGGTGCGGA
GGGGCGTGTGTGCCGGCGCGCGCCGTGGGGTGCAAACCCCGAGCGCTCTACGCTGCCATGA
GGGGCGGAAACGCCTGGGGCGCACTCTGCCTGTCTGGCTGCCGCCACCCAGCTCTCCGGG
CAGCAGTCCCCAGAGAGACTGTTTTACATGTGGTGGCATTCTTACTGGAGAGTCTGGATT
TATTGGCAGTAAGGTTTTCTGGAGTGTACCCTCCAAATAGCAAATGTACTTGGAAATCA
CAGTTCGCCAAGGAAAAGTAGTCGTTCTCAATTTCCGATTATAGACCTCGAGAGTGACAAC
CTGTGCCGTATGACTTTGTGGATGTGTACAATGGCCATGCCAATGGCCAGCGCATTTGGCCG
CTTCTGTGGCACTTTCCGGCCTGGAGCCCTTGTGTCCAGTGGCAACAAGATGATGGTGCAGA
TGATTTCTGATGCCAACACAGCTGGCAATGGCTTCATGGCCATGTTCTCCGCTGTGTAACCA
AACGAAAGAGGGGATCAGTATTGTGGAGGACTCCTTGACAGACCTTCGGCTCTTTTAAAC
CCCCAAGTGGCCAGACCGGGATTACCTTGACAGGAGTCACTTGTGTGTGGCACATTGTAGCCC
CAAAGAATCAGCTTATAGAATTAAAGTTTGAAGAAGTTTGATGTGGAGCGAGATAACTACTGC
CGATATGATTATGTGGCTGTGTTAATGGCGGGGAAGTCAACGATGTAGAGAATTTGGAAA
GTATTGTGGTGATAGTCCACCTGCGCAATTGTGTCTGAGAGAATGAACCTCTTATTTCAGT
TTTTATCAGACTTAAGTTTAACTGCAGATGGGTTTATTGGTCACTACATATTTCAGGCCAAAA
AACTGCCTACAACCTACAGAACAGCCTGTCAACACCATTTCCCTGTAAACACGGGTTTTAAA
ACCCACCGTGGCCCTTGTGTCAACAAAAGTGTAGACGGACGGGGACTCTGGAGGGCAATTATT
GTTCAAGTGACTTTGTATTAGCCGGCACTGTTATCAACCATCACTCGCGATGGGAGTTTG
CAGCCACAGTCTCGATCATCAACATCTACAAAGAGGGAAATTTGGCGATTTCAGCAGGCGGG
CAAGAACATGAGTGCCAGGCTGACTGTCGTCTGCAAGCAGTGCCTCTCCTCAGAAGAGGTC
TAAATTACATTATTATGGGCCAAGTAGGTGAAGATGGGCGAGGCAAAATCATGCCAAACAGC
TTTATCATGATGTTCAAGACCAAGAATCAGAAGCTCCTGGATGCCTTAAAAAATAAGCAATG
TTAAACAGTGAAGTGTGCCATTTAAGCTGTATTCTGCCATTGCCTTTGAAAGATCTATGTTT
TCTCAGTAGAAAAAAAATACTTATAAAATTACATATTCTGAAGAGGATTCCGAAAGATGG
GACTGGTGTACTCTTCAATGATGGAGGTATGAGGCCTCCGAGATAGCTGAGGGAAGTTCTT
TGCCGTGTGTGACAGGAGCAGCTATCTGATTGGAAACCTGCCACTTAGTGCAGTGTATAGGA
AGCTAAAAGTGTCAAGCGTTGACAGCTTGGAAAGCGTTTATTATTACATCTCTGTAAAAGGAT
ATTTTAGAATTGAGTGTGTGAAGATGTCAAAAAAGATTTTAGAAGTGCATATTATTATAGT
GTTATTGTGTTTCACTTCAAGCCTTTGCCCTGAGGTGTTACAATCTTGTCTGCGTTTTCTTA
AATCAATGCTTAATAAAATATTTTTAAAGGAAAAA

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FIGURE 38

MRGANAWAPLCLLLAAATQLSRQQSPERPVFTCGGILTGESGFIGSEGFPGVYPNSKCTWK
ITVPEGKVVVLNFRFIDLESDNLCRYDFVDVYNHANGQRIGRFCGTFRPGALVSSGNKMMV
QMISDANTAGNGFMAMFSAAEPNERGDQYCGLLDRPSGSFKTPNWPDRDYPAGVTCVWHIV
APKNQLIELKFEKFDVERDNYCRYDYVAVFNGGEVNDARRIGKYCGDSPPAPIVSEARNELLI
QFLSDLSTADGFIGHYIFRPKKLPTTTEQPVTTTTFPVTTGLKPTVALCQCKRRTGTLEGN
YCSSDFVLAGTVITITRDGSLHATVSIINIYKEGNLAIQQAGKNMSARLTVVCKQCPLLR
GLNYIIMGQVGEDGRGKIMPNSFIMMFKTKNQKLLDALKNKQC

Signal sequence:

amino acids 1-23

N-glycosylation site.

amino acids 355-359

Casein kinase II phosphorylation site.

amino acids 64-68, 142-146, 274-278

Tyrosine kinase phosphorylation site.

amino acids 199-208

N-myristoylation site.

amino acids 34-40, 35-41, 100-106, 113-119, 218-224, 289-295,
305-311, 309-315, 320-326, 330-336

Cell attachment sequence.

amino acids 149-152

FIGURE 39

CGGACGCGTGGGCGGACGCGTGGGCGGCCACGGCGCCCGCGGGCTGGGGCGGTGCGCTTCTT
CCTTCTCCGTGGCCTACGAGGGTCCCCAGCCTGGGTAAAGATGGCCCCATGGCCCCGAAGG
GCCTAGTCCCAGCTGTGCTCTGGGGCCTCAGCCTCTTCCTCAACCTCCCAGGACCTATCTGG
CTCCAGCCCTCTCCACCTCCCAGTCTTCTCCCCGCGCTCAGCCCCATCCGTGTGCATACCTG
CCGGGGACTGGTTGACAGCTTTAAACAAGGGCCTGGAGAGAACCATCCGGGACAACTTTGGAG
GTGGAACAACCTGCTGGGAGGAAGAGAATTTGTCCAATACAAGACAGTGAGACCCGCCTG
GTAGAGGTGCTGGAGGGTGTGTGCAGCAAGTCAGACTTCGAGTGCCACCGCCTGTCTGGAGCT
GAGTGAGGAGCTGGTGGAGAGCTGGTGGTTTCAAGCAGCAGGAGGCCCGGACCTCTTCC
AGTGGCTGTGCTCAGATTCCCTGAAGCTCTGCTGCCCGCGCAGGCACCTTCGGGCCCTCCTGC
CTTCCCTGTCTGGGGGAACAGAGAGGCCCTGCGGTGGCTACGGGCAGTGTGAAGGAGAAGG
GACACGAGGGGGCAGCGGCCTGTGACTGCCAAGCCGGCTACGGGGGTGAGGCCCTGTGGCC
AGTGTGGCCTTGGCTACTTTGAGGCAGAACGCAACGCCAGCCATCTGGTATGTTTCGGCTTGT
TTTGGCCCTGTGCCGATGCTCAGGACCTGAGGAATCAAACCTGTTTGAATGCAAGAAGGG
CTGGCCCTGCATCACCTCAAGTGTGTAGACATTGATGAGTGTGGCACAGAGGGAGCCAAC
GTGGAGCTGACCAATTCTGCGTGAACACTGAGGGCTCCTATGAGTGCCGAGACTGTGCCAAG
GCCTGCCTAGGTGCATGGGGGCAGGGCCAGGTGCTGTAAGAAGTGTAGCCCTGGCTATCA
GCAGGTGGGCTCCAAGTGTCTCGATGTGGATGAGTGTGAGACAGAGGTGTGTCGGGAGAGA
ACAAGCAGTGTGAAAACACCGAGGGCGGTTATCGTGCATCTGTGCCGAGGGCTACAAGCAG
ATGGAAGGCATCTGTGTGAAGGAGCAGATCCAGAGTCAGCAGGCTTCTTCTCAGAGATGAC
AGAAGACGAGTTGGTGGTGTGTCAGCAGATGTTCTTTGGCATCATCATCTGTGCACTGGCCA
CGCTGGCTGCTAAGGGCGACTTGGTGTTCACCGCCATCTTCATTGGGGCTGTGGCGGCCATG
ACTGGCTACTGGTTGTGAGAGCGCAGTGACCGTGTGCTGGAGGGCTTCATCAAGGGGAGATA
ATCGCGGCCACACCTGTAGGACCTCCTCCCACCCACGCTGCCCCAGAGCTTGGGTGCC
TCCTGTCTGGACACTCAGGACAGCTTGGTTTATTTTGGAGAGTGGGGTAAGCACCCTACCTG
CCTTACAGAGCAGCCAGGTACCCAGGCCCGGGCAGACAAGGCCCTGGGGTAAAAAGTAGC
CCTGAAGGTGGATACCATGAGCTCTTACCTGGCGGGGACTGGCAGGCTTCACAATGTGTGA
ATTTCAAAGTTTTCTTAATGGTGGCTGCTAGAGCTTTGGCCCCCTGCTTAGGATTAGGTG
GTCCTCAGAGGGTGGGGCCATCACAGCTCCCTCCTGCCAGCTGCATGCTGCCAGTTCCTGT
TCTGTGTTTACCACATCCCCACACCCCATTTGCCACTTATTTATTCATCTCAGGAAATAAAGA
AAGGTCTTGGAAAGTTAAAAA

FIGURE 40

MAPWPPKGLVPAVLWGLSLFLNLP GPIWLQPSPPQSSPPFPQPHPCHTCRGLVDSFNKGLER
TIRDNFGGGNTAWEENLSKYKDSETRLVEVLEGVCSKSDFECHRLLELSEELVESWWFHKQ
QEAPDLFQWLCSDSLKCCPAGTFGPSCLPCPGGTERPCGGYGQCEGEGTRGGSGHCDQAG
YGGACGQCGLGYFEARNASHLVCSACFGPCARCSGPEESNCLQCKKGWALHHLKCVDIDE
CGTEGANCGADQFCVNTEGSYECRDCAKACLGCMGAGPGRCKKCSPGYQQVGSKCLDVDECE
TEVCPGENKQCENTEGGYRCICAEGYKQMEGICVKEQIPESAGFFSEMTEDELVVLLQQMFFG
IIICALATLAAKGDLVFTAIFIGAVAAMTGYWLSERSDRVLEGFIKGR

Signal sequence:

amino acids 1-29

Transmembrane domain:

amino acids 372-395

N-glycosylation site.

amino acids 79-83, 205-209

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 290-294

Casein kinase II phosphorylation site.

amino acids 63-67, 73-77, 99-103, 101-105, 222-226, 359-263

N-myristoylation site.

amino acids 8-14, 51-57, 59-65, 69-75, 70-76, 167-173, 173-179,
177-183, 188-194, 250-256, 253-259, 267-273, 280-286, 283-289,
326-332, 372-378, 395-401

Aspartic acid and asparagine hydroxylation site.

amino acids 321-333

EGF-like domain cysteine pattern signature.

amino acids 181-193

Year	Age	Sex	Height (cm)	Weight (kg)	Body Mass Index (kg/m ²)	Waist Circumference (cm)	Waist-Hip Ratio	Trunk Fat (%)	Visceral Fat (cm ³)	Subcutaneous Fat (cm ³)	Visceral Fat Index (cm ³ /m ²)	Subcutaneous Fat Index (cm ³ /m ²)
2001	25	M	175	75	24.5	95	0.95	15	150	100	0.9	0.6
2002	26	M	176	78	24.8	96	0.96	16	160	110	0.9	0.6
2003	27	M	177	80	25.1	97	0.97	17	170	120	0.9	0.6
2004	28	M	178	82	25.4	98	0.98	18	180	130	0.9	0.6
2005	29	M	179	84	25.7	99	0.99	19	190	140	0.9	0.6
2006	30	M	180	86	26.0	100	1.00	20	200	150	0.9	0.6
2007	31	M	181	88	26.3	101	1.01	21	210	160	0.9	0.6
2008	32	M	182	90	26.6	102	1.02	22	220	170	0.9	0.6
2009	33	M	183	92	26.9	103	1.03	23	230	180	0.9	0.6
2010	34	M	184	94	27.2	104	1.04	24	240	190	0.9	0.6
2011	35	M	185	96	27.5	105	1.05	25	250	200	0.9	0.6
2012	36	M	186	98	27.8	106	1.06	26	260	210	0.9	0.6
2013	37	M	187	100	28.1	107	1.07	27	270	220	0.9	0.6
2014	38	M	188	102	28.4	108	1.08	28	280	230	0.9	0.6
2015	39	M	189	104	28.7	109	1.09	29	290	240	0.9	0.6
2016	40	M	190	106	29.0	110	1.10	30	300	250	0.9	0.6
2017	41	M	191	108	29.3	111	1.11	31	310	260	0.9	0.6
2018	42	M	192	110	29.6	112	1.12	32	320	270	0.9	0.6
2019	43	M	193	112	29.9	113	1.13	33	330	280	0.9	0.6
2020	44	M	194	114	30.2	114	1.14	34	340	290	0.9	0.6
2021	45	M	195	116	30.5	115	1.15	35	350	300	0.9	0.6
2022	46	M	196	118	30.8	116	1.16	36	360	310	0.9	0.6
2023	47	M	197	120	31.1	117	1.17	37	370	320	0.9	0.6
2024	48	M	198	122	31.4	118	1.18	38	380	330	0.9	0.6
2025	49	M	199	124	31.7	119	1.19	39	390	340	0.9	0.6
2026	50	M	200	126	32.0	120	1.20	40	400	350	0.9	0.6
2027	51	M	201	128	32.3	121	1.21	41	410	360	0.9	0.6
2028	52	M	202	130	32.6	122	1.22	42	420	370	0.9	0.6
2029	53	M	203	132	32.9	123	1.23	43	430	380	0.9	0.6
2030	54	M	204	134	33.2	124	1.24	44	440	390	0.9	0.6
2031	55	M	205	136	33.5	125	1.25	45	450	400	0.9	0.6
2032	56	M	206	138	33.8	126	1.26	46	460	410	0.9	0.6

TTGAGACCCCTCCTGCAGCCTTCTCAAGGGACAGCCCCACTCTGCCTCTTGCTCCTCCAGGGCA
 GCACCATGCAGCCCCCTGTGGCTCTGCTGGGCACTCTGGGTGTTGCCCTGGCCAGCCCCGGG
 GCCGCCCTGACCGGGGAGCAGCTCCTGGGCAGCCTGCTGCGGCAGCTGCAGCTCAAGAGAGGT
 GCCACCCCTGGACAGGGCCGACATGGAGGAGCTGGTCATCCCCACCCACGTGAGGGCCCCAGT
 ACGTGGCCCTGCTGCAGCGCAGCCACGGGGACCGTCCCGCGGAAGAGGTTTCAGCCAGAGC
 TTCGAGAGAGGTGGCCGGCAGGTTCTTGGCGTTGGAGGGCCAGCACACCTGCTGGTGTTTCGG
 CATGAGCAGCGGCTGCCGCCCAACAGCGAGCTGGTGCAGGCCGTGCTGCGGCTCTTTCAGG
 AGCCGGTCCCCAAGGCCGCGCTGCACAGGCACGGGCGGTCTGCCCGCGCAGCGCCCCGGGCC
 CGGGTGACCGTCGAGTGGCTGCGCGTCCGCGACGACGGCTCCAACCGCACCTCCCTCATCGA
 CTCACGGCTGGTGTCCTGCCACGAGAGCGGCTGGAAGGCCTTCGACGTGACCGAGGCCGTGA
 ACTTCTGCGCAGCAGCTGAGCCGGCCCCGCGCAGCCGCTGCTGCTACAGGTGCTCGGTGCAGAGG
 GGCATCTGGGCTCCGCTGGCGCTCCGCGCCCAACAAGCTGGTCCGCTTTGCTTCGACGGGGCC
 GACACGCCGGCTTGGGAGCGCCCGAGCTGGAGCTGAGCACTGCACACCTTGCTTTGGGGACATGAGG
 CTCAGGGCGACTGTGACCCTGAAGCACCAATGACCGAGGGCACCCGCTGCTGCGGCCAGAG
 ATGTACATTGACCTGCAGGGGATGAAGTGGGCCGAGAAGTGGGTGCTGGAGCCCCCGGGCTT
 CCTGGCTTATGAGTGTGTGGGCACCTGCCCGCAGCCCCCGGAGGCCCTGGCCTTCAAGTGGC
 CGTTTCTGGGGCTTCGACAGTGCATCGCCTCGGAGACTGACTCGTGCCCATGATCGTCAGC
 ATCAAGGAGGGAGGCAGGACCAGGCCCCAGGTGGTCAGCCTGCCCAACATGAGGGTGCAGAA
 GTGCAGCTGTGCCTCGGATGGTGCCTCGTGCCAAGGAGGCTCCAGCCATTAGCGCCCTAGTG
 TAGCCATCGAGGGACTTGACTTGTGTGTGTTTCTGAAGTGTTTCGAGGGTACCAGGAGAGCTG
 GCGATGACTGAACGTCTGATGGACAAATGCTCTGTGCTCTCTAGTGAGCCCTGAATTGCTT
 CCTCTGACAAGTTACCTCACCTAAATTTTTGCTTCTCAGGAATGAGAATCTTTGGCCACTGGA
 GAGCCCTTGCTCAGTTTTCTCTATTCTTATTATTCACTGCATATATTTCAAGCACTTACAT
 GTGGAGATACTGTAACCTGAGGGCAGAAAGCCANTGTGTCAATTGTTTACTTGTCTCTGTAC
 TGTCTCTGGGCTAAAGTCCTCCACCACCACTCTGGACCTAAGACCTGGGGTTAAGTGTGGGT
 TGGATCATCCCCAATCCAGATAATAAAGACTTTGTAAAAATCATGAATAAAACACATTTTATTCT
 AAAA

FIGURE 42

MQPLWLCWALWVLPLASPGAALTGEQLLGSLLRQLQLKEVPTLDRADMEELVIPTHVRAQYV
ALLQRSHGDRSRGKRFSQSFEVAGRFLALEASTHLLVFGMEQRLPPNSELVQAVLRLFQEP
VPKAALHRHGRLSFRSARARVTVEWLVRDDGSNRTSLIDSRLVSVHESGWKAFDVTEAVNF
WQQLSRPRQPLLLQVSVQREHLGPLASGAHKLVRFASQGAPAGLGEPQLELHTLDLGDYGAQ
GDCEPEAPMTEGTRCCRQEMYIDLQGMKWAENWVLEPPGFLAYECVGTCTCRQPPEALAFKWPF
LGPRQCIASETDSLPMIVSIKEGGRTRPQVVSLPNMRVQKCSASCSDGALVPRRLQP

Signal sequence:

amino acids 1-18

N-glycosylation site.

amino acids 158-162

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 76-80

Casein kinase II phosphorylation site.

amino acids 68-72, 81-85, 161-165, 169-173, 319-323, 329-333

N-myristoylation site.

amino acids 19-25, 156-162, 225-231, 260-266, 274-280

Amidation site.

amino acids 74-78

TGF-beta family signature.

amino acids 282-298

FIGURE 43

GTCTGTTCCAGGAGTCCTTCGGCGGCTGTTGTGTGTCAGTGGCCTGATCGCGATG~~GGG~~GACAAA
GGCGCAAGTCGAGAGGAAACTGTTGTGCTCTTCATATTGGCGATCCTGTTGTGCTCCCTGG
CATTGGGCAGTGTACAGTGCACCTCTTCTGAACCTGAAGTCAGAATTCCTGAGAATAATCCT
GTGAAGTTGTCTGTGCCTACTCGGGCTTTTCTTCTCCCCGTGTGGAGTGGAAAGTTTGACCA
AGGAGACACCACCAGACTCGTTTGCTATAATAACAAGATCACAGCTTCCTATGAGGACCGGG
TGACCTTCTTGCCAACCTGGTATCACCTTCAAGTCCGTGACACGGGAAGACACTGGGACATAC
ACTTGTATGTGCTCTGAGGAAGGCGGCAACAGCTATGGGGAGGTCAAGGTCAAGCTCATCGT
GCTTGTGCCTCCATCCAAGCCTACAGTTAACATCCCCCTCCTCTGCCACCATTTGGGAACCGGG
CAGTGTGACATGCTCAGAACAAGATGGTTCACCTTCTGAATACACCTGGTTCAAAGAT
GGGATAGTGTATGCTACGAATCCCAAAAGCACCCGTCGCTTCAGCAACTCTTCTATGTCTCT
GAATCCCAACAACAGGAGAGCTGGTCTTTGATCCCTGTGAGCTCTGATACTGGAGAATACA
GCTGTGAGGCACGGAATGGGTATGGGACACCATGACTTCAAATGCTGTGCGCATGGAAGCT
GTGGAGCGGAATGTGGGGGTGTCATCGTGGCAGCCGTCCTTGTAACTTGAATTCCTCGGGAAAT
CTTGGTTTTTGGCATCTGGTTTGCTATAGCCGAGGCCACTTTGACAGAACAAGAAAGGGA
CTTCGAGTAAGAAGGTGATTACAGCCAGCCTAGTGCCCAAGTGAAGGAGAATTCAAACAG
ACCTCGTCATTCTGGTGTG~~AG~~AGCCTGGTCGGCTCACCGCCTATCATGTGCATTGCGCTTACT
CAGGTGTACCGGACTCTGGCCCTGATGTCTGTAGTTTACAGGATGCCTTATTTGTCTTC
TACACCCACAGGGCCCCCTACTTCTTCGGATGTGTTTTAATAATGTCAGCTATGTGCCCC
ATCTCTCTTCATGCCCTCCCTCCCTTTCCTACCACTGCTGAGTGGCTGGAACCTGTTTTAAA
GTGTTTATTCCTCATTTCTTTGAGGGATCAGGAAGGAATCCTGGGTATGCCATTGACTTCCC
TTCTAAGTAGACAGCAAAATGCGGGGGTGCAGGAATCTGCACTCAACTGCCACCTGGC
TGGCAGGGATCTTTGAATAGGTATCTTGAGCTTGGTTCTGGGCTCTTTCTTGTGTACTGAC
GACCAGGGCCAGCTGTTCTAGAGCGGGAATTAGAGGCTAGAGCGGTGAAATGGTTGTTTGG
TGATGACACTGGGGTCTTCCATCTCTGGGGCCCACTCTCTTCTGTCTTCCATGGGAAGTG
CCACTGGGATCCCTCTGCCTGTCTCTCTGAATACAAGCTGACTGACATTGACTGTGTCTGT
GGAAAATGGGAGCTCTTGTGTGGAGAGCATAGTAAATTTTCAGAGAACTGAAGCCAAAAG
GATTTAAAACCGCTGCTCTAAAGAAAAGAAAACCTGGAGGCTGGGCGCAGTGGCTCACGCCTG
TAATCCAGAGGCTGAGGCAGGCGGATCACCTGAGGTGCGGAGTTGCGGATCAGCCTGACCA
ACATGGAGAAACCTACTGGAATACAAAGTTAGCCAGGCATGGTGGTGCATGCCTGTAGTC
CCAGCTGCTCAGGAGCCTGGCAACAAGAGCAAACTCCAGCTCAAAAAAAAAAAAAAAAAA

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FIGURE 44

MGTKAQVERKLLCLFILAILLCSLALGSVTVHSSEPEVRIPENNPVKLS CAYS GFSSPRVEW
KFDQGD TTRLVCYNNKITASYEDRVTF LPTGITFKSVTREDTGT YTCMVSEEGGNSYGEVKV
KLIVLVPPSKPTVNI PSSATIGNRAVLTCSEQDGSPPSEYTWFKDGIVMPTNPKSTRAFSNS
SYVLNPTTGELVFDPLSASDTGEYSCEARNGYGT PMTSNAVRMEAVERNVGVIVA AVLVTLI
LLGILVFGIWFAYS RGHFDR TKKGTS SKKVIYSQPSARSEGEFKQTSSFLV

Signal sequence:

amino acids 1-27

Transmembrane domain:

amino acids 238-255

N-glycosylation site.

amino acids 185-189

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 270-274

Casein kinase II phosphorylation site.

amino acids 34-38, 82-86, 100-104, 118-122, 152-156, 154-158,
193-197, 203-207, 287-291

N-myristoylation site.

amino acids 105-111, 116-122, 158-164, 219-225, 237-243, 256-262

FIGURE 45

CAGCGCGTGGCCGGCGCCGCTGTGGGGACAGC**ATG**AGCGGCGGTTGGATGGCGCAGGTTGGAGCGTGGCGAACAGGGGCTCTGGGCCCTGGCGCTGCTGCTGCTCGGCCCTCGGACTAGGCCTGGAGGCCCGCCGCGAGCCCGCTTTCACCCCGACCTCTGCCCAGGCCGCGAGGCCCAGCTCAGGCTCGTGCCACCCACCAAGTTCCAGTGCCGCACCAAGTGCGCTTATGCGTGCCCTCACCTGGCGCTGCGACAGGGACTTGGACTGCGAGCGATGGCAGCGATGAGGAGGAGTGCAGGATTGAGCCATGTACCCAGAAAGGGCAATGCCACCGCCCCCTGGCCTCCCCTGCCCCTGACCGCGCTCATGTACTGCTCTGGGGGAACTGACAAGAAACTGCGCAACTGCAGCCGCTGGCCTGCCTAGCAGGCGAGCTCCGTTGCACGCTGAGCGATGACTGCATTCCACTCACGTGGCGCTGCGACGGCCA CCCAGACTGTCCCGACTCCAGCGACGAGCTCGGCTGTGGAAACCAATGAGATCCTCCCGGAAGGGGATGCCACAACCATGGGGCCCCCTGTGACCCTGGAGAGTGTACCTCTCTCAGGAATGCCACAACCATGGGGCCCCCTGTGACCCTGGAGAGTGTCCCCCTCTGTCGGGAATGCCACATCCTCTCTGCGCGAGACCAGTCTGGAAGCCCAACTGCCCTATGGGGTTATTGCAGCTGCTGCGGTGCTCAGTGCAAGCCTGGTCACCGCCACCTCCTCCTTTTGTCCTGGCTCCGAGCCAGGAGCGCCTCCGCCCACTGGGGTTACTGTTGGCCATGAAGGAGTCCCTGCTGCTGTGAGAACAGAAGACTCGCTGCCCC**TGA**GGACAAGCACTTGCCACCACCGTCACTAGCCCTGGGCGTAGCCGGACAGGAGAGAGCAGTGATGCGGATGGGTACCCGGGCACACCAGCCCTCAGAGACCTGAGTTCTTCTGGCCACGTGGAACCTCGAACCCGAGCTCCTGCAGAAGTGGCCCTGGAGATTGAGGGTCCC TGGACACTCCCTATGGAGATCCGGGGAGCTAGGATGGGGAACTGCCACAGCCAGAACTGAGGGGTGGCCCCAGGCAGCTCCAGGGGGTAGAACGGCCCTGTGCTTAAGACTCCTCGCTGCCCCGTCTGAGGGTGCGATTAAAGTTGCTTC

660573 07101

FIGURE 46

MSGGWMAQVGAWRTGALGLALLLLGLGLGLEAAASPLSTPTSQAAGPSSGSCPPTKFKQCR
TSGLCVPLTWRCDRDLDCSDGSDEEECRIEPCTQKGQCPPPGLPCPCTGVSDCSGGTDKKL
RNC SRLACLAGE LRCTLSDDCIPLTWRC DGHPCPDSSDELGCCTNEILPEGDATTMGPPVT
LESVTSLRNATTMGPPVTLESVPSVGNATSSSAGDQSGSPTAYGVIAAAVLSASLVTATLL
LLSWLRAQERLRPLGLLVAMKESLLLSQKTSLP

Signal sequence:

amino acids 1-30

Transmembrane domain:

amino acids 230-246

N-glycosylation site.

amino acids 126-130, 195-199, 213-217

Casein kinase II phosphorylation site.

amino acids 84-88, 140-144, 161-165, 218-222

N-myristoylation site.

amino acids 3-9, 10-16, 26-32, 30-36, 112-118, 166-172, 212-218,
224-230, 230-236, 263-269

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 44-55

Leucine zipper pattern.

amino acids 17-39

FIGURE 47

CCCACGCGTCCGGTCTCGCTCGCTCGCGCAGCGGCGGCAGCAGAGGTCGCGCACAGATGCGG
GTTAGACTGGCGGGGGGAGGAGGCGGAGGAGGGAAGGAAGCTGCATGCATGAGACCCACAGA
CTCTTGCAAGCTGGATGCCCTCTGTGGATGAAAGATGTATCATGGAATGAACCCGAGCAATG
GAGATGGATTTC TAGAGCAGCAGCAGCAGCAGCAGCAACCTCAGTCCCCCAGAGACTCTTG
GCCGTGATCCTGTGTTTCAGCTGGCGCTGTGCTTCGGCCCTGCACAGCTCACGGGCGGGTT
CGATGACCTTCAAGTGTGTGCTGACCCCGGCATTCCCGAGAATGGCTTCAGGACCCCCAGCG
GAGGGGTTTTCTTTGAAGGCTCTGTAGCCCGATTTCACTGCCAAGACGGATTCAAGCTGAAG
GGCGCTACAAAGAGACTGTGTTTGAAGCATTTTAATGGAACCTTAGGCTGGATCCCAAGTGA
TAATTCATCTGTGTGCAAGAAGATTGCCGTATCCCTCAAATCGAAGATGCTGAGATTCATA
ACAAGACATATAGACATGGAGAGAAGCTAATCATCACTTGTTCATGAAGGATTCAAGATCCGG
TACCCCGACCTACACAATATGGTTTCATTATGTGCGGATGATGGAACGTGGAATAATCTGCC
CATCTGTGCAAGGCTGCCTGAGACCTCTAGCCTCTTCTAATGGCTATGTAAACATCTCTGAGC
TCCAGACCTCCTTCCCGGTGGGACTGTGATCTCCTATCGCTGCTTTCCCGGATTAAACTT
GATGGGTCTGCGTATCTTGAGTGCTTACAAAACCTTATCTGGTCGTCAGCCACCCCGGTG
CCTTGCTCTGGAAGCCCAAGTCTGTCCACTACCTCCAATGGTGAGTCACGGAGATTTCGTCT
GCCACCCGCGGCTTGTGAGCGCTACAACCACGGAACGTGTGGAGATTTTACTGCGATCCT
GGCTACAGCCTACCCAGCGACTACAAGTACATCACCTGCCAGTATGGAGAGTGGTTTCTTTC
TTATCAAGTCTACTGCATCAAATCAGAGCAAACGTGGCCGACGACCCATGAGACCTCCTGA
CCACGTGGAAGATTGTGGCGTTCACGGCAACCAGTGTGCTGCTGGTGTGCTGCTCGTCATC
CTGGCCAGGATGTTCCAGACCAAGTTC AAGGCCACTTTCCCCCAGGGGCGCTCCCGGAG
TTCCAGCAGTGACCTGACTTTGTGGTGGTAGACGGCGTGCCCGTCATGCTCCCGTCCTATG
ACGAAGCTGTGAGTGGCGGCTTGAGTGCCTTAGGCCCGGGTACATGGCCTCTGTGGGCCAG
GGCTGCCCTTACCCGTGGACGACAGAGCCCCCAGCATACCCGGCTCAGGGGACACGGA
CACAGGCCCAGGGGAGTCAGAAACCTGTGACAGCGTCTCAGGCTCTTCTGAGCTGCTCCAAA
GTCTGTATTACCTCCAGGTGCCAAGAGAGCACCACCTGCTTCGGACAACCTTGACATA
ATTGCCAGCACGGCAGAGGAGGTGGCATCCACAGCCCCAGGCATCCATCATGCCCACTGGGT
GTGTTCCTAAGAAACTGATTGATTAAAAAATTTCCCAAAGTGTCTGAAAGTGTCTCTTCAA
ATACATGTTGATCTGTGGAGTTGATTCTTTCTTCTCTGGTTTTAGACAAATGTAACAA
AGCTCTGATCCTTAAATTGCTATGCTGATAGAGTGGTGAGGCTGGAAGCTTGATCAAGTC
CTGTTTCTCTTGACACAGACTGATTAAAAATTAAGNAAAAA

FIGURE 48

MYHGMNPSNGDGFLEQQQQQQPQSPQRLLAVILWFLALCFGPAQLTGGFDDLQVCADPGI
PENGFRTPSGGVFFEGSVARFHCQDGFKLKGATKRLCLKHFNGTLGWIPSDNSICVQEDCRI
PQIEDAEIHNKTYRHGEKLIITCHEGFKIRYPDLHNMMVSLCRDDGTWNNLPICQGCLRPLAS
SNGYVNISELQTSFFPVGTVISYRCFPGFKLDGSAYLECLQNLIIWSSSPPRCLALEAQVCPLP
PMVSHGDFVCHPRPCERYNHGTVVEFYCDPGYSLTSDYKYITCQYGEWFPSPYQVYCIKSEQT
WPSTHETLLTTWKIVAFTATSVLLVLLLVILARMFQTKFKAHFPPRGPPRSSSSDPDFVVVD
GVPVMLPSYDEAVSGGLSALGPGYMASVGQGCPLPVDDQSPPAYPGSGD TDTGPGESETCDS
VSGSSELLQSLYSPPRCQESTHPASDNPDIIASTAEVASTSPGIHHAHWLFLRN

Signal sequence:

amino acids 1-41

Transmembrane domain:

amino acids 325-344

N-glycosylation site.

amino acids 104-108, 134-138, 192-196

Casein kinase II phosphorylation site.

amino acids 8-12, 146-150, 252-256, 270-274, 313-317, 362-366,
364-368, 380-384, 467-471, 468-472

N-myristoylation site.

amino acids 4-10, 61-67, 169-175, 203-209, 387-393, 418-424,
478-484

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 394-405

FIGURE 49

CCCACGCGTCCGCTCCGCGCCCTCCCCCGCCTCCCGTGCGGTCCGTCCGTGGCCTAGAGA
TGCTGCTGCCGCGGTTGCAGTTGTGCGCGCACGCCTCTGCCCGCCAGCCCGCTCCACCGCGT
AGCGCCCGAGTGTCCGGGGGCGCACCCGAGTCGGGCCATGAGGCCGGGAACCGCGCTACAGG
CCGTGCTGCTGGCCGTGCTGCTGGTGGGGCTGCGGGCCGCGACGGGTGCGCTGCTGAGTGCC
TCGGATTTGGACCTCAGAGGAGGGCAGCCAGTCTGCCGGGGAGGGACACAGAGGCCCTTGTTA
TAAAGTCATTTACTTCCATGATACTTCTCGAAGACTGAACCTTTGAGGAAGCCAAAGAAGCCT
GCAGGAGGGATGGAGGCCAGCTAGTCAGCATCGAGTCTGAAGATGAACAGAACTGATAGAA
AAGTTCATTGAAAACCTCTTGCCATCTGATGGTGACTTCTGGATTGGGCTCAGGAGGCGTGA
GGAGAAACAAAGCAATAGCACAGCCTGCCAGGACCTTTATGCTTGGACTGATGGCAGCATAT
CACAAATTAGGAACTGGTATGTGGATGAGCCGTCTCGCGGACGCGAGGTCTGCGTGGTCATG
TACCATCAGCCATCGGCACCCGCTGGCATCGGAGGCCCTACATGTTCCAGTGGAATGATGA
CCGGTGCAAACATGAAGAACAAATTTCAATTGCAAATATTTGATGAGAAACAGCAGTTCCTT
CTAGAGAAGCTGAAGGTGAGGAAACAGAGCTGACAACACCTGTACTTCCAGAAGAAACACAG
GAAGAAGATGCCAAAAAACATTTAAAGAAAGTAGAGAAGCTGCCTTGAATCTGGCCTACAT
CCTAATCCCCAGCATTCCCCTTCTCCTCCTCTGTGGTCACCACAGTTGTATGTTGGGTTT
GGATCTGTAGAAAAAGAAAACGGGAGCAGCCAGACCCTAGCACAAAGAAGCAACACACCATC
TGCCCTCTCCTCACCAGGGAAACAGCCCGGACCTAGAGGTCTACAATGTCATAAGAAAACA
AAGCGAAGCTGACTTAGCTGAGACCCGCCAGACCTGAAGAATATTTCAATCCGAGTGTGTT
CGGGAGAAGCCACTCCCGATGACATGTCTTGTGACTATGACAACATGGCTGTGAACCCATCA
GAAAGTGGGTTTGTGACTCTGGTGAGCGTGAGAGTGGAATTTGTGACCAATGACATTATGA
GTTCTCCCAGACCAATGGGGAGGAGTAAGGAGTCTGGATGGGTGGAAAATGAAATATATG
GTTATTAGGACATATAAAAAAAGTAAACTGACAAACATGGAAAAAGAAATGATAAGCAAAATC
CTCTATTTTCTATAAGGAAAAATACACAGAAGGTCTATGAACAAGCTTAGATCAGGTCCTGT
GGATGAGCATGTGGTCCCCACGACCTCCTGTTGGACCCCCACGTTTTGGCTGTATCCTTTAT
CCAGCCAGTCATCCAGCTCGACCTTATGAGAAGGTACCTTGCCAGGTCTGGCACATAGTA
GAGTCTCAATAAATGTCACTTGGTTGGTTGTATCTAACTTTTAAGGGACAGAGCTTTACCTG
GCAGTGATAAAGATGGGCTGTGGAGCTTGGAACACCACTCTGTTTTCCTGCTCTATACAG
CAGCACATATTATCATACAGACAGAAAATCCAGAATCTTTTCAAAGCCACATATGGTAGCACAG
GTTGGCTGTGCATCGGCAATTCTCATATCTGTTTTTTTCAAAGAATAAAATCAAATAAAGA
GCAGGAAAAA

FIGURE 50

MRPGTALQAVLLAVLLVGLRAATGRLLSASDLDLRGQPVCRGGTQRPCYKVIYFHDTSRRL
NFEEAKEACRRDGGQLVSI ESEDEQKLI EKFIENLLPSDGD FWIGLRRREEKQSNSTACQDL
YAWTDGSI SQFRN WYVDEPSCGSEVCVVMYHQPSAPAGIGGPYMFQWNDDRCNMKNNFICKY
SDEKPAVPSREAEGETELTTPVLPEETQEEDAKKTFKESREAAALNLAYILIPSIPLLLLLV
VTVVVCVWVICRKRKREQPD PSTKKQHTIWPSPHQGNSPDLEVYNVIRKQSEADLAETRPDL
KNISFRVCSGEATPD DMSCDYDNMAVNPSES GFVTLSVESG FVTNDIYEFSPDQMGRSKES
GWVENEIYGY

Signal sequence:

amino acids 1-21

Transmembrane domain:

amino acids 235-254

N-glycosylation site.

amino acids 117-121, 312-316

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 296-300

Casein kinase II phosphorylation site.

amino acids 28-32, 30-34, 83-87, 100-104, 214-218, 222-226,
299-303, 306-310, 323-327

N-myristoylation site.

amino acids 18-24, 37-43, 76-82, 146-152

	Age	Sex	Height cm	Weight kg	BMI	Waist cm	Hip cm	WHR	SBP mmHg	DBP mmHg	Pulse b/min	Fasting glucose mg/dl	HbA _{1c} %	Insulin mU/ml	C-peptide ng/ml	OGTT-0 min	OGTT-60 min	OGTT-120 min	OGTT-180 min	OGTT-240 min	OGTT-300 min	OGTT-360 min	OGTT-420 min	OGTT-480 min	OGTT-540 min	OGTT-600 min	OGTT-660 min	OGTT-720 min	OGTT-780 min	OGTT-840 min	OGTT-900 min	OGTT-960 min	OGTT-1020 min	OGTT-1080 min	OGTT-1140 min	OGTT-1200 min	OGTT-1260 min	OGTT-1320 min	OGTT-1380 min	OGTT-1440 min	OGTT-1500 min	OGTT-1560 min	OGTT-1620 min	OGTT-1680 min	OGTT-1740 min	OGTT-1800 min	OGTT-1860 min	OGTT-1920 min	OGTT-1980 min	OGTT-2040 min	OGTT-2100 min	OGTT-2160 min	OGTT-2220 min	OGTT-2280 min	OGTT-2340 min	OGTT-2400 min	OGTT-2460 min	OGTT-2520 min	OGTT-2580 min	OGTT-2640 min	OGTT-2700 min	OGTT-2760 min	OGTT-2820 min	OGTT-2880 min	OGTT-2940 min	OGTT-3000 min	OGTT-3060 min	OGTT-3120 min	OGTT-3180 min	OGTT-3240 min	OGTT-3300 min	OGTT-3360 min	OGTT-3420 min	OGTT-3480 min	OGTT-3540 min	OGTT-3600 min	OGTT-3660 min	OGTT-3720 min	OGTT-3780 min	OGTT-3840 min	OGTT-3900 min	OGTT-3960 min	OGTT-4020 min	OGTT-4080 min	OGTT-4140 min	OGTT-4200 min	OGTT-4260 min	OGTT-4320 min	OGTT-4380 min	OGTT-4440 min	OGTT-4500 min	OGTT-4560 min	OGTT-4620 min	OGTT-4680 min	OGTT-4740 min	OGTT-4800 min	OGTT-4860 min	OGTT-4920 min	OGTT-4980 min	OGTT-5040 min	OGTT-5100 min	OGTT-5160 min	OGTT-5220 min	OGTT-5280 min	OGTT-5340 min	OGTT-5400 min	OGTT-5460 min	OGTT-5520 min	OGTT-5580 min	OGTT-5640 min	OGTT-5700 min	OGTT-5760 min	OGTT-5820 min	OGTT-5880 min	OGTT-5940 min	OGTT-6000 min	OGTT-6060 min	OGTT-6120 min	OGTT-6180 min	OGTT-6240 min	OGTT-6300 min	OGTT-6360 min	OGTT-6420 min	OGTT-6480 min	OGTT-6540 min	OGTT-6600 min	OGTT-6660 min	OGTT-6720 min	OGTT-6780 min	OGTT-6840 min	OGTT-6900 min	OGTT-6960 min	OGTT-7020 min	OGTT-7080 min	OGTT-7140 min	OGTT-7200 min	OGTT-7260 min	OGTT-7320 min	OGTT-7380 min	OGTT-7440 min	OGTT-7500 min	OGTT-7560 min	OGTT-7620 min	OGTT-7680 min	OGTT-7740 min	OGTT-7800 min	OGTT-7860 min	OGTT-7920 min	OGTT-7980 min	OGTT-8040 min	OGTT-8100 min	OGTT-8160 min	OGTT-8220 min	OGTT-8280 min	OGTT-8340 min	OGTT-8400 min	OGTT-8460 min	OGTT-8520 min	OGTT-8580 min	OGTT-8640 min	OGTT-8700 min	OGTT-8760 min	OGTT-8820 min	OGTT-8880 min	OGTT-8940 min	OGTT-9000 min	OGTT-9060 min	OGTT-9120 min	OGTT-9180 min	OGTT-9240 min	OGTT-9300 min	OGTT-9360 min	OGTT-9420 min	OGTT-9480 min	OGTT-9540 min	OGTT-9600 min	OGTT-9660 min	OGTT-9720 min	OGTT-9780 min	OGTT-9840 min	OGTT-9900 min	OGTT-9960 min	OGTT-10020 min	OGTT-10080 min	OGTT-10140 min	OGTT-10200 min	OGTT-10260 min	OGTT-10320 min	OGTT-10380 min	OGTT-10440 min	OGTT-10500 min	OGTT-10560 min	OGTT-10620 min	OGTT-10680 min	OGTT-10740 min	OGTT-10800 min	OGTT-10860 min	OGTT-10920 min	OGTT-10980 min	OGTT-11040 min	OGTT-11100 min	OGTT-11160 min	OGTT-11220 min	OGTT-11280 min	OGTT-11340 min	OGTT-11400 min	OGTT-11460 min	OGTT-11520 min	OGTT-11580 min	OGTT-11640 min	OGTT-11700 min	OGTT-11760 min	OGTT-11820 min	OGTT-11880 min	OGTT-11940 min	OGTT-12000 min	OGTT-12060 min	OGTT-12120 min	OGTT-12180 min	OGTT-12240 min	OGTT-12300 min	OGTT-12360 min	OGTT-12420 min	OGTT-12480 min	OGTT-12540 min	OGTT-12600 min	OGTT-12660 min	OGTT-12720 min	OGTT-12780 min	OGTT-12840 min	OGTT-12900 min	OGTT-12960 min	OGTT-13020 min	OGTT-13080 min	OGTT-13140 min	OGTT-13200 min	OGTT-13260 min	OGTT-13320 min	OGTT-13380 min	OGTT-13440 min	OGTT-13500 min	OGTT-13560 min	OGTT-13620 min	OGTT-13680 min	OGTT-13740 min	OGTT-13800 min	OGTT-13860 min	OGTT-13920 min	OGTT-13980 min	OGTT-14040 min	OGTT-14100 min	OGTT-14160 min	OGTT-14220 min	OGTT-14280 min	OGTT-14340 min	OGTT-14400 min	OGTT-14460 min	OGTT-14520 min	OGTT-14580 min	OGTT-14640 min	OGTT-14700 min	OGTT-14760 min	OGTT-14820 min	OGTT-14880 min	OGTT-14940 min	OGTT-15000 min	OGTT-15060 min	OGTT-15120 min	OGTT-15180 min	OGTT-15240 min	OGTT-15300 min	OGTT-15360 min	OGTT-154
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GGGGTCTCCCTCAGGGCCGGGAGGCACAGCGGTCCCTGCTTGCTGAAGGCTGGATGTACGC
ATCCGCAGGTTCCCGCGGACTTGGGGGCGCCCGCTGAGCCCCGGCGCCCGCAGAAGACTTGT
GTTTGCCCTCTGCAGCCTCAACCCGAGGGCAGCGAGGGCCTACCACCATGATCACTGGTGT
GTTACGATGCGCTTGTTGGACCCCACTGGGCGTCTTGACCTCGCTGGCGTACTGCTGCACC
AGCGGCGGGTGGCCCTGGCCGAGCTGCAGGAGGCCGATGGCCAGTGTCCGGTCGACCCGAGC
CTGCTGAAGTTGAAAATGGTGCAGGTCGTGTTTCGACACGGGGCTCGGAGTCCTCTCAAGCC
GCTCCCGCTGGAGGAGCAGGTAGAGTGGAACCCCACTATTAGAGGTCCCACCCCAAATCT
AGTTTGATTACACAGTCACCAATCTAGCTGGTGGTCCGAAACCATATTCTCCTTACGACTCT
CAATACCATGAGACACCCTGAAGGGGGGCATGTTTGTGGCAGCTGACCAAGTGGGCAT
CGACGAAATGTTGCCCTTGGGAGAGAGATCGAGGAAGACTATGTGAAGACATTTCCCTTTC
TTTCAACACCTTTCAACCCAGAGGAGTCTTTATTCGTTCACATAACATTTTTCGGAATCTG
GAGTCCACCCGTTGTTTGCTGGCTGGGCTTTTCCAGTGTCAGAAAGAAGGACCATCATCAT
CCACACTGATGAAGCAGATTCAAGTCTTGATCCCAACTACCAAAGCTGCTGGAGCCTGA
GGCAGAGAAACAGAGGCCGGAGGCAGACTGCCTCTTTACAGCCAGGAATCTCAGAGGATTG
AAAAAGGTGAAGGACAGGATGGGCATTGACAGTAGTGATAAAGTGGACTTCTTCATCCTCCT
GGACAACGTGGCTGCCGAGCAGGCACACAACCTCCCAAGCTGCCCATGCTGAAGAGATTG
CACGGATGATCGAACAGAGAGCTGTGGACACATCCTTGTACATACTGCCCAAGGAAGACAGG
GAAAGTCTTCAGATGGCAGTAGGCCATTCTCCACATCCTAGAGAGCAACCTGCTGAAAGC
CATGGACTCTGCCACTGCCCCCGACAAGATCAGAAAGCTGTATCTCTATGCGGCTCATGATG
TGACCTTCATACCGCTCTTAATGACCTGGGGATTTTTGACCACAATGGCCACCGTTTGCT
GTTGACCTGACCATTGGAACTTTACCAGCACCTGGAATCTAAGGAGTGGTTTGTGCAGCTCTA
TTACCACGGGAAGGACAGGTGCCGAGAGGTTGCCCTGATGGGCTCTGCCCGCTGGACATGT
TCTTGAATGCCATTGAGTTTATACCTTAAGCCCGAAAAATACCATGCACTCTGCTCTCAA
ACTCAGGTGATGGAAGTTGAAATGAAGAGTAACTGATTATAAAAGCAGGATGTGTTGATT
TTAAATAAAGTGCCCTTTATACAATG

FIGURE 52

MITGVFSMRLWTPVGVLTSLAYCLHQRRVALAELQEADGGQCPVDRSLLKLMVQVVFRHGAR
SPLKPLPLEEQVEWNPQLLEVPPQTQFDYTVTNLAGGPKPYSPYDSQXHETTLKGGMFAGQL
TKVGMQOMFALGERLARKNYVEDIPFLSPTFNPQEVFIRSTNIFRNLESTRCLLAGLFQCQKE
GPIIIHTDEADSEVLYPNYQSCWSLRQTRGRRQTASLQPGISEDLLKKVKDRMGIDSSDKVD
FFILLDNVAAEQAHNLPSCPMLKRFRMIEQRAVDTSLYILPKEDRESLQMAVGPFPHILES
NLLKAMDSATAPDKIRKLYLYAAHDVTFIPLMLTLGIFDHKWPPFAVDLTMELYQHLESKEW
FVQLYYHGKEQVPRGCPDGLCPLDMFLNAMSVYTLSPKEYHALCSQTQVMEVGNEE

Signal sequence:

amino acids 1-23

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 218-222

Casein kinase II phosphorylation site.

amino acids 87-91, 104-108, 320-324

Tyrosine kinase phosphorylation site.

amino acids 280-288

N-myristoylation site.

amino acids 15-21, 117-123, 118-124, 179-185, 240-246, 387-393

Amidation site.

amino acids 216-220

Leucine zipper pattern.

amino acids 10-32

Histidine acid phosphatases phosphohistidine signature.

amino acids 50-65

FIGURE 53

CTCCTCTTAACATACTTGCAGCTAAAACTAAATATTGCTGCTTGGGGACCTCCTTCTAGCCT
TAAATTTTCAGCTCATCACCTTCACCTGCCTTGGTCATGGCTCTGCTATTCTCCTTGATCCTT
GCCATTTTGACACAGACCTGGATTCTTAGCGTCTCCATCTGGAGTGGCGCTGGTGGGGGGCCT
CCACCGCTGTGAAGGGCGGTGGAGGTGGAACAGAAAGGCCAGTGGGGCACCCTGTGTGATG
ACGGCTGGGACATTAAAGGACGTGGCTGTGTTGTGCCGGGAGCTGGGCTGTGGAGCTGCCAGC
GGAACCCCTAGTGGTATTTTGTATGAGCCACCAGCAGAAAAAGAGCAAAAGGTCCCTCATCCA
ATCAGTCAGTTGCACAGGAACAGAAGATACATTGGCTCAGTGTGAGCAAGAAGAAGTTTATG
ATTGTTACATGATGAAGATGCTGGGGCATCGTGTGAGAACCCAGAGAGCTCTTTCTCCCA
GTCCAGAGGGTGTGAGGCTGGCTGACGGCCCTGGGCATTGCAAGGGACGCGTGGAAGTGAA
GCACCAGAACCAAGTGGTATACCGTGTGCCAGACAGGCTGGAGCCTCCGGGCCGCAAAAGGTGG
TGTGCCGGCAGCTGGGATGTGGGAGGGCTGACTGACTCAAAAAACGCTGCAACAAGCATGCC
TATGGCCGAAAAACCATCTGGCTGAGCCAGATGTCATGCTCAGGACGAGAAGCAACCCTTCA
GGATTGCCCTTCTGGGCCTTGGGGGAAGAACACCTGCAACCATGATGAAGACACGTGGGTCTG
AATGTGAAGATCCCTTTGACTTGAGACTAGTAGGAGGAGACAACCTCTGCTCTGGGCGACTG
GAGGTGCTGCACAAGGGCGTATGGGGCTCTGTCTGTGATGACAACTGGGGAGAAAAGGAGGA
CCAGGTGGTATGCAAGCAACTGGGCTGTGGGAAGTCCCTCTCTCCCTCCCTTCAGAGACCGGA
AATGCTATGGCCCTGGGGTTGGCCGCATCTGGCTGGATAATGTTTCGTGCTCAGGGGAGGAG
CAGTCCCTGGAGCAGTGCCAGCACAGATTTTGGGGGTTTACGACTGCACCCACCAGGAAGA
TGTGGCTGTCTGCTCAGTGTAGGTGGGCATCATCTAATCTGTTGAGTGCCTGAATAGAA
GAAAAACACAGAAGAAGGGAGCATTTACTGTCTACATGACTGCATGGGATGAACACTGATCT
TCTTCTGCCCTTGGACTGGGACTTATACTTGGTGCCCTGATTCTCAGGCCCTTCAGAGTTGG
ATCAGAACCTTACAACATCAGGTCTAGTTCTCAGGCCATCAGACATAGTTTGGAACTACATCA
CCACCTTTCCCTATGTCTCCACATTGCACACAGCAGATTTCCAGCCCTCCATAATTGTGTGTAT
CAACTACTTAAATACATTCTCACACACACACACACACACACACACACACACACAT
ACCATTTTGTCCTGTTCTCTGAAGAACTCTGACAAAATACAGATTTTGGTACTGAAAGAGA
TTCTAGAGGAACGGAATTTTAAAGATAAAATTTTCTGAATTGGTTATGGGGTTTCTGAAATTG
GCTCTATAATCTAATTAGATATAAAATTTCTGGTAACCTTTATTTACAATAATAAGATAGCAC
TATGTGTTCAAA

FIGURE 54

MALLFSLILAICTRPGFLASPSGVRLVGGLHRCGRVEVEQKGQWGTVCDDGWDIKDVAVLC
RELCCGAASGTFPSGILYEPPAEKEQKVLIQSVSCTGTEDTLAQCEQEVEYDCSHDEDAGASC
ENPESSSFSPVPBGVRLADGPGHCKGRVEVKHQNQWYTVQCQTGWSLRAAKVVCRLGCGRAVL
TQKRCNKHAYGRKPIWLSQMCSGREATLQDCPSGPWGKNTCNHDEDTWVECEDPFDLRLVG
GDNLCSGRLEVLHKGVWGSVCDDNWGEKEDQVVCKQLGCGKSLSPSFRDRKCYGPGVGRIWL
DNVRCSGEEQSLEQCQHRFWGFHDCTHQEDVAVICSV

Signal sequence:

amino acids 1-15

Casein kinase II phosphorylation site.

amino acids 47-51, 97-101, 115-119, 209-213, 214-218, 234-238,
267-271, 294-298, 316-320, 336-340

N-myristoylation site.

amino acids 29-35, 43-49, 66-72, 68-74, 72-78, 98-104, 137-143,
180-186, 263-269, 286-292

Amidation site.

amino acids 196-200

Speract receptor repeated domain signature.

amino acids 29-67, 249-287

FIGURE 55

ACTGCACTCGGTTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCCTCGACCTCGAC
CCACGCGTCCGCGGACGCGTGGGCGGACGCGTGGGCCGGCTACCAGGAAGAGTCTGCCGAAG
GTGAAGGCCATGGACTTTCATCACCTCCACAGCCATCCTGCCCTGCTGTTTCGGCTGCCTGGG
CGTCTTCGGCCTCTTCGGGTGCTGCAGTGGGTGCGCGGGAAGGCCTACCTGCGGAATGCTG
TGGTGGTGATCACAGGCGCCACCTCAGGGCTGGGCAAGAATGTGCAAAAGTCTTCTATGCT
GCGGTGCTAAACTGGTGCTCTGTGGCCGGAATGGTGGGGCCCTAGAAAGAGCTCATCAGAGA
ACTTACCCTTCTCATGCCCACCAAGGTGCAGACACACAAGCCTTACTTGGTGACCTTCGACC
TCACAGACTCTGGGGCCATAGTTGCAGCAGCAGCTGAGATCCTGCAGTGCTTTGGCTATGTC
GACATACTTGTCAACAATGCTGGGATCAGCTACCGTGGTACCATCATGGACACCACAGTGGA
TGTGGACAAGAGGGTCATGGAGACAAACTACTTTGGCCAGTTGCTCTAACGAAAGCACTCC
TGCCCTCCATGATCAAGAGGAGGCAAGGCCACATTGTGCGCCATCAGCAGCATCCAGGGCAAG
ATGAGCATTCCTTTTCGATCAGCATATGCAGCCTCCAAGCACGCAACCAGGCTTTCTTTGA
CTGTCTGCGTGCCGAGATGGAAACAGTATGAAATTGAGGTGACCGTCATCAGCCCCGGCTACA
TCCACACCAACCTCTCTGTAAATGCCATCACCGCGGATGGATCTAGGTATGGAGTTATGGAC
ACCACCACAGCCAGGGCCGAAGCCCTGTGGAGGTGGCCAGGATGTTCTTGCTGCTGTGGG
GAAGAAGAAGAAAGATGTGATCCTGGCTGACTTACTGCCTTCCTTGGCTGTTTATCTTCGAA
CTCTGGCTCCTGGGCTCTTCTTCAGCCTCATGGCCTCCAGGGCCAGAAAAGAGCGGAAATCC
AAGAACTCCTAGTACTCTGACCAGCCAGGGCCAGGGCAGAGAAGCAGCACTCTTAGGCTTGC
TTACTCTACAAGGGACAGTTGCATTTGTTGAGACTTAAATGGAGATTTGTCTCAAGTGGG
AAAGACTGAAGAAACACATCTCTGCAGATCTGCTGGCAGAGGACAATCAAAAACGACAACA
AGCTTCTTCCCAGGGTGAGGGGAAACACTTAAGGAATAAATATGGAGCTGGGGTTTAAACT
AAAAACTAGAAATAAACATCTCAACAGTAAAAAAGGGCGGCCGCACTCTAG
AGTCGACCTGCAGAAGCTTGGCCCGCATGGCCCAACTTGTATTGACAGCTTATAATGGTTAC

FIGURE 56

MDFITSTAILPLLFGCLGVFGLFRLLQWVRGKAYLRNAVVVITGATSGLGKECAKVFYAAGA
KLVLCGRNGGALEELIRELTASHATKVQTHKPYLVTFDLTDSGAIVAAAAEILQCFGYVDIL
VNNAGISYRGTIMDITVDVDRVMETNYFGPVALTKALLPSMIKRRQGHIVAIISSIQGKMSI
PFRSAYAASKHATQAFDFCLRAEMEQYEIEVTVISPGYIHTNLSVNAITADGSRYGVMDDTTT
AQGRSPVEVAQDVLAAVGGKKKDVILADLLPSLAVYLRTLAPGLFFSLMASRARKERKSKNS

Signal sequence:

amino acids 1-21

Transmembrane domain:

amino acids 104-120, 278-292

N-glycosylation site.

amino acids 228-232

Glycosaminoglycan attachment site.

amino acids 47-51

Casein kinase II phosphorylation site.

amino acids 135-139, 139-143, 253-257

Tyrosine kinase phosphorylation site.

amino acids 145-153, 146-153

N-myristoylation site.

amino acids 44-50, 105-111, 238-244, 242-248, 291-297

Amidation site.

amino acids 265-269

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 6-17

FIGURE 57

CCCACGCGTCCGCTGGTGTAGATCGAGCAACCTCTAAAAGCAGTTTAGAGTGGTAAAAAA
AAAAAAAACACACCAAACGCTCGCAGCCACAAAAGGGATGAAATTTCTTCTGGACATCCTC
CTGCTTCTCCGTTACTGATCGTCTGCTCCCTAGAGTCTTCGTGAAGCTTTTTATTCTTAA
GAGGAGAAAATCAGTACCGGCGAAATCGTGCTGATTACAGGAGCTGGGCATGGAATTGGGA
GACTGACTGCCTATGAATTTGCTAACTTAAAAGCAAGCTGGTTCTCTGGGATATAAATAAG
CATGGACTGGAGGAAACAGCTGCCAAATGCAAGGGACTGGGTGCCAAGGTTCATACCTTTGT
GGTAGACTGCAGCAACCGAGAAGATATTACAGCTCTGCAAGAAGGTGAAGGCAGAAAATG
GAGATGTTAGTATTTTAGTAAATAATGCTGGTGTAGTCTATACATCAGATTTGTTTGTCTACA
CAAGATCCTCAGATTGAAAAAGACTTTTGAAGTTAATGTACTTGACATTTCTGGACTACAAA
GGCATTTCTTCTGCAATGACGAAGAATAACCATGGCCATATTGTCACTGTGGCTTCGGCAG
CTGGACATGTCTCGGTCCCTTCTTACTGGCTTACTGTTCAAGCAAGTTTGTCTGTGTTGGA
TTTCATAAAACTTTGACAGATGAACTGGCTGCCCTTACAAATAACTGGAGTCAAAACACATG
TCTGTGTCTCTAATTTGTAACACTGGCTTCATCAAAAATCCAAGTACAAGTTTGGGACCCA
CTCTGGAACTTGAGGAAGTGTTAAACAGGCTGATGCATGGGATTCTGACTGAGCAGAAGATG
ATTTTTATTCCATCTTCTATAGCTTTTTTAACAACATTGGAAAGGATCCTTCTGAGCGTTT
CCTGGCAGTTTTAAACGAAAAATCAGTGTTAAGTTTGATGCAGTTATTGGATATAAAATGA
AAGCGCAATAAGCACCTAGTTTTCTGAAAACGTATTACCAGGTTTAGGTTGATGTCATCTA
ATAGTGCCAGAATTTAATGTTTGAACCTCTGTTTTTCTAATTATCCCCATTTCTTCAATA
TCATTTTGTAGGCTTTGGCAGTCTTCATTTACTACCACTGTTCCTTTAGCCAAAAGCTGATT
ACATATGATATAAACAGAGAAATACCTTTAGAGGTGACTTTAAGGAAAATGAAGAAAAGAA
CCAAAATGACTTTATTAAAATAAATTCGAAGATTATTGTGGCTCACCTGAAGGCTTTGCCAA
AATTGTACCATAACCGTTTATTAAACATATATTTTATTTTTGATTGCACTTAAATTTTGT
ATAATTTGTGTTTCTTTTCTGTTCTACATAAAATCAGAACTTCAAGCTCTCTAAATAAAA
TGAAGGACTATATCTAGTGGTATTTCAATGAATATCATGAACTCTCAATGGGTAGGTTTC
ATCTACCCATTGCCACTCTGTTTCTGAGAGATACCTCACATTCCAATGCCAAACATTTCT
GCACAGGGAAGCTAGAGGTGGATACAGTGTGCAAGTATAAAAGCATCACTGGGATTAAAG
GAGAATTGAGAGAAATGATCCACAAATGGCAGCAATAATAAATGGATCACACTTAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

00002572-071001

FIGURE 58

MKFLLDILLLLPLLIVCSLESFVKLFIPKRRKSVTGEIVLITGAGHGIGRLTAYEFAKLKSK
LVLWDINKHGLEETAACKCKGLGAKVHTFVVDCSNREDIYSSAKVKAEIGDVSILVNNAGVV
YTSDLFATQDPQIEKTFEVNVLAHFWTTKAFLPAMTKNNHGHIVTVASAAGHVSVPFLLAYC
SSKFAAVGFHKLTLTDELAALQITGVKTTCLCPNFVNTGFIKNPSTSLGPTLEPEEVNRLMH
GILTEQKMIFIPSSIAFLTLERILPERFLAVLKRKISVKFDDAIVIGYKMKAQ

Signal sequence:

amino acids 1-19

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 30-34, 283-287

Casein kinase II phosphorylation site.

amino acids 52-56, 95-99, 198-202, 267-271

N-myristoylation site.

amino acids 43-49, 72-78, 122-128, 210-216

[illegible]

CCACACGCGTCCGCGGCGCGCTGGGTGCAGTACGTTCTAGATCGCGAGCGGGCCGCCCGCGGCTC
AGGGAGGAGCACCAGCATCGCCGCGCCCTCGAGAGATCGGGTGGTCCATGTGGGAAGGTGATGTT
TTTCGCTGGTCTCTTGATGCTCGTGGCCCTGTGATGGGTGTTTTCGCTCCCTATACAGAAGT
GTTTCCATGCCACCTCAAGGGAGACTCAGGACAGCCATTATTTCCACCCCTTACATTGAAGC
TGGGAAGATCCAAAGAAGAGAAATTTAGTTTTGGTTCGGCCCTTTCCAGGACTGAAACATGA
AGAGTTATGCCGGCTTCCTCACCGTGAATAAGACTTCAACACGACAACTCTTCTCTGGTTT
TTCCAGCTCAGATACAGCCAGAGAAGTAGCCCGCATGATGTTCTCTGGCTACAGGGTGGGCGGG
AGGTTCTATCATGTTTGGATCTTTTGTGGAACATGGGCCCTATGTTGTGTCACAAGTAACTAGA
CCTTGCCTGACAGAGACTTCCCTCGGACCAACAGCTCTCCATGCTTTACATTGACAATCCA
TGGGCGCACAGGCTTCAGTTTTACTGATGATACCCAGGATATGCAGTCAATAGGAGGCAGTGT
AGCACGGGATTTATACAGTGACATAATTTCAGTTTTCCAGATATTTCTGAATATTAATAATA
ATGACTTTTATGTCACTGGGAGTCTTATGCGAGGAATAATTGTGCCAGCCATTGCAACCTC
ATCCATTCCTCAACCTCTGTGAGAGAGTGGAAGTCAACCTGAACGGAATTTGCTATTGGAGA
TGGATATTTCTGATCCCGAATCAATTAAGGGGGCTATGCAGAATTCCTGTACCAAAATTTGGCT
TGTTGGATGAGAAGCAAAAAGATCTTCCAGAGCAGTGCCATGAATGCATAGAACACATC
AGGAAGCAGAAGCTGGTTTGGAGCCCTTGAAGACTCATGGTAACATACTAGTAGGGCAGCTTAAC
AAGTAGCTCTTCTTACTTCCAGAATGTTACAGGATGTAGTAATTACTATACTCTTTTGGCGGT
GCACGGAACCTTAGGATCAGCTTTACTATTGGAATTTTGTCTACCTCCAGAGCTTGAGACAA
GCCATCCAGTGGGGAAATCAGACTTTTAATGATGGAATTTATGTTGAAAGTACTTGCAGGA
AGATACAGTACAGCTCAGTTAAGCCTAGGTTAACATGAAATCATGAATTAATTAAGGTTCTGA
TCTCAATGGGCCAATGGACATCTCGTGGCAGCTGCCCTGACAGAGCGCTTTCTGATGGCG
ATGGAATGGAAGGATCCCGAGGATAACAAGAAGGCAGAAAAAAAGTTTGAAGATCTTTAA
ATCTGACAGTGAAAGTGGCTGGTTACATCCGGCAGCGGGTGACTCCATCAGGTAAATTTCT
GAGGTGGAGGACATATTTTACCCTATGACAGCCTCTGAGAGCTTTTGACATGATTAATCGA
TTCATTTTGGAAAAGGATGGGATCCTTATGTTGGGATTAAGTACCTTCCCAAAAGAGAACAT
CAGAGGTTTTCTATGCTGAAAAGAAATCGTAAACAGAAATGTCAAGGAATTAATAAA
TTATCTTTTTCATATCTGCAAGATTTTTTTCATCAATAAAAAATTTCTTGAACCAAGTGAGC
TTTTTTTGGGGGGAGATGTTTACTACAAAATTAACATGAGTACATGATGAATTAACATTA
TTATTTAACTTAAGAGCTGAAGGTATGGATGATGTGACATGAGACAGATGATGATTAAGATGA
AATTTTAGGCTCTGAATAGGAAGTTTAAATTTCTTCTAAGAGTAAGTGAAGAAAGTGCAAGTTG
TAACAAACAAAGCTGTAACATCTTTTTCTGCCAATAACAGAGAGTTTGGCATGCGGTGAAGGT
GTTTGGAAATATTATTGGATAAGAATAGCTCAATTTCCCAATAAATGGATGAAGCTATAA
TAGTTTGTGGGAAAAGATTTCAATGTATAAAGTCTTGAACCAAAAAGAAATTTCTTGAATAA
AAAAATATTATATATAAAGTAAAAAAA

FIGURE 60

MVGAMWKVIVSLVLLMPGCDGLFRSLYRSVSMPPKGDGQPLFLTPYIEAGKIQKGRELSL
VGPPFGLNMKSYAGFLTIVNKTYNSNLFFWFFPAQIQPEDAPVVLWLQGGPGGSSMFGLFVEH
GPYVVTSNMTLDRDFPWTTLTSLMLYIDNPVGTGFSFTDDTHGYAVNEDDVARDLYSALIQT
FQIFPEYKNNDFYVTGESYAGKYVPAIAHLIHS LNPNVREV KINLNGIAIGDGYSDPESIIGG
YAEFLYQIGLLDEKQKKYFQKQCHECIEHIRKQNWFEAFEILDKLLDGLTSDPSYFQNVGT
CSNYYNFLRCTEPEDQLYVVKFLSLPEVRQAIHVGNQTFNDGTIVEKYLREDTVQSVKPWLT
EIMNNYKVLIIYNGQLDIIVAAALTE RSLMGMDWKGSQ EYKKA EKVKWIKFKSDSEVAGYIRQ
AGDFHQVIIRGGGHILPYDQPLRAFDMINRFIYGKGDWPYVG

Signal sequence:

amino acids 1-22

N-glycosylation site.

amino acids 81-85, 132-136, 307-311, 346-350

Casein kinase II phosphorylation site.

amino acids 134-138, 160-164, 240-244, 321-325, 334-338, 348-352,
353-357, 424-428

Tyrosine kinase phosphorylation site.

amino acids 423-432

N-myristoylation site.

amino acids 22-28, 110-116, 156-162, 232-238

Serine carboxypeptidases, serine active site.

amino acids 200-208

Crystallins beta and gamma 'Greek key' motif signature.

amino acids 375-391

FIGURE 61

CGAGGGCTTTTCCGGCTCCGGAATGGCACATGTGGGAATCCCACTCTTGTGTGGCTACAACAT
TTTTCCCTTTCTCAACAAGTTCTAACAGCTGTTCTAACAGCTAGTGATCAGGGGTTCTTCTT
GCTGGAGAAGAAAGGGCTGAGGGCAGAGCAGGGCACTCTCACTCAGGGGTGACCAAGCTCCTTG
CCTCTCTGTGGATAACAGAGCATGAGAAAGTGAAGAGATGCAGCGGAGTGAGGTGATGGAAG
TCTAAAATAGGAAGGAATTTTGTGTGCAATATCAGACTCTGGGAGCAGTTGACCTGGAGAGC
CTGGGGGAGGGGCTGCCTAAACAAGCTTTCAAAAAACAGGAGCGACTTCCACTGGGCTGGGAT
AAGACGTGCCGGTAGGATAGGGAAGACTGGGTTTAGTCTCTAATATCAAATTGACTTGCTGGG
TGAACCTTCAAAGCCTTTTAACTCTCTGGGAGATGAAAACGATGGCTTAAAGGGCCAGAAA
TAGAGATGCTTTGTAATAATAAATTTAAAAAAGCAAGTATTTTATAGCATAAAGGCTAGA
GACCAAAATAGATAACAGGATTCCTGAACTTCTTAAGAGGGAGAAAGTATGTTAAAAATA
GAAAAACCAAATGCAGAAGGAGGAGACTCACAGAGCTAAACAGGATGGGGACCCCTGGGTC
AGGCCAGCCTCTTTGCTCCTCCCGAAATATTTTTGGTCTGACCACTCTGCCTTGTGTTTT
GCAGAAATCATGTGAGGGCCAAACCGGGGAAGGTGGAGCAGATGAGCACACACAGGAGCCGTCT
CCTCACCGCCGCCCCCTCTCAGCATGGAACAGAGGCAGCCCTGGCCCCGGGCCCTGGAGGTGG
ACAGCCGCTCTGTGGTCTGTCTCAGTGGTCTGGGTGCTGCTGGCCCCCAGCAGCCGGC
ATGCCCTCACTTCAAGCCTTCCACTCTGAGAATCGTGACTGGAACCTTCAACCACTTGACCGT
CCACCAAGGGACGGGGGCGGTCTATGTGGGGCCATCAACCGGGTCTATAAGCTGACAGGCA
ACCTGACCATCCAGGTGGCTCATAAGACAGGGCCAGAAGAGGACAACAAGTCTCGTTACCCG
CCCTCATCGTGCAGCCCTGCAGCGAAGTGCTCACCTCACCAACAATGTCAACAAGCTGCT
CATCATTGACTACTCTGAGAACCGCCTGCTGGCCTGTGGGAGCCTCTACAGGGGGTCTGCA
AGCTGCTCGGCTGGATGACCTCTTCATCCTGGTGGAGCCATCCCAAGAAGGAGCACTAC
CTGTCCAGTGTCAACAAGACGGGCACCATGTACGGGGTGATGTGCGCTTGAGGGGTGAGGA
TGGAAGCTCTTCATCGGCACGGCTGTGGATGGGAAGCAGGATTACTTCCGACCCCTGTCCA
GCCGAAGCTGCCCGAGACCCTGAGTCTCAGCCATGCTCGACTATGAGCTACACAGCGAT
TTTGCTCTCTCTCATCAAGATCCCTTCAGACACCCTGGCCCTGGTCTCCCACTTTTGACAT
CTTCTACATCTACGGCTTTGTCTAGTGGGGGCTTTGTCTACTTTCTCACTGTCCAGCCCGAGA
CCCTGAGGGTGTGGCCATCAACTCCGCTGGAGACCTCTTCTACACCTCAGCATCTGTGCGG
CTCTGCAAGGATGACCCCAAGTTCACCTCATACGTGTCCTTGCCCTTCGGCTGCACCCGGGC
CGGGGTGGAATAACCGCTCTCTGCAGGCTGCTTACCTGGCCAAGCCTGGGACTCACTGGCCC
AGGCCTTCAATATCACCAGCCAGGACGATGTACTCTTTGCCATCTTCTCAAAGGGCAGAAG
CAGTATCACCACCCGCCCCGATGACTCTGCCCTGTGTGCCTTCCCTATCCGGGCCATCAACTT
GCAGATCAAGGAGCGCTGCAGTCTCTGCTACCAGGCGAGGGCAACCTGGAGCTCAACTGGC
TGCTGGGGAAGGACGTCAGATGCACGAAGGCGCCTGTCCCATCGATGATAACTTCTGTGGA
CTGGACATCAACCAGCCCCCTGGGAGGCTCAACTCCAGTGGAGGGCCTGACCTGTACACCAC
CAGGAGGACCGCATGACCTCTGTGGCTCCTACGTTTACAACGGCTACAGCGTGGTGGTTTTG
TGGGCACTAAGAGTGGAAGCTGAAAAAGGTAAAGTCTATGAGTTTCAGATGCTCCAATGCC
ATTCACTCTCAGCAAAAGAGTCCCTCTTGAAGGTAGCTATTGGTGAGATTAACTATAG
GCAACTTTATTTTCTTGGGGAACAAAGGTGAATGGGAGGTAAAGAAGGGTTAATTTTGTG
ACTTAGCTTCTAGCTACTTCTCCAGCCATCAGTCATTGGGTATGTAAGGAATGCAAGCGTA
TTTCAATATTTCCCAAACCTTAAAGAAAAAAGCTTAAAGAAGGTACATCTGCAAAAGCAA

FIGURE 62

MGTLGQASLFAPPNGYFWSHDHSAFCFAESCEGQPGKVEQMSTHRSRLTLTAAPLSMEQRQPWP
RALEVDSRSVVLSSVWVLLAPPAAGMPQFSTFHSENRDWTFNHLTVHQGTGAVYVGAINRV
YKLTGNLTIQVAHKTGPEEDNKSRYPLIVQPCSEVLTLTNVNVKLLIIDYSENRLACGSL
YQGVCKLLRLDDLFIIVEPSSHKEHYLSSVNKTGTMYGVIVRSEGEDGKLFITAVDGKQDY
FPFLSSRKLPRDPSSAMLDYELHSDFFVSSLIKIPSDTLALVSHFDIFYIYGFAAGGFVYFL
TVQPETPEGVAINSAGDLFYTSRIVRLCKDDPKFHSYVSLPFGCTRAGVEYRLLQAAYLAKP
GDSLAFQAFNITSQDDVLFALFISKGQKQYHHPDDSDALCAFPPIRAINLQIKERLQSCYQGEGN
LELNWLLGKDVQCTKAPVPIDDFCGLDINQPLGGSTPVEGLTLYTTSRDRMTSVASYVYNG
YSVVFVGTKSGKLLKVRVYEFRCNSNAIHLLSKESLLEGSYWWRFNRYQLYFLGEQR

Signal sequence:

amino acids 1-32

Transmembrane domain:

amino acids 71-87

N-glycosylation site.

amino acids 130-134, 145-149, 217-221, 381-385

Casein kinase II phosphorylation site.

amino acids 139-143, 229-233, 240-244, 291-295, 324-328, 383-387,
384-388, 471-475, 481-485, 530-534

N-myristoylation site.

amino acids 220-226, 319-325, 353-359, 460-466, 503-509

[illegible][illegible]

FIGURE 64

MTTWSLRRRPPARTLGLLLLVLGFLVLRRLDWSTLVPLRLRHRQLGLQAKGWNFMLEDSTFW
IFGGSIHYFRVPREYWRDRLKMKACGLNTLTYYVPWNLHEPERGKFDGSGNLDLEAFVLMA
AIGLWVILRPGPYICSEMDLGGPLPSWLLQDPGMRLRTTYKGFTAVDLYFDHLSRVVPLQ
YKRGPIIAVQVENEYGSYNKDPAYMPYVKKALEDRGIVELLTSDNKDGLSKGIVQGVLAT
INLQSTHELQLLTTFLFNVQGTQPKMVMYWTGWFDSWGPHNILDSSVLTQVSAIVDAGS
SINLYMFHGGTNGFGFMNGAMHFHDYKSDVTSYDYDAVLTEAGDYTAKYMKLRDFFGSISGIP
LPPPPDLLPKMPYEPPLTPVLYLSLWDALKYLGEPIKSEKPINMENLPVNGNGQSFGYILYE
TSITSSGILSGHVHDRGQVFVNTVSIQFLDYKTTKIAVPLIQGYTVLRILVENRGRVNYGEN
IDDQRKGLIGNLYLNDSPKKNFRIYSLDMKKSFFQRFGLDKWXSPLPETPTLPAPFFLGSLSSIS
STPCDTFLKLEGWEKGVVFINGQNLGRYWNIGPQKTLTYLPGFWLSSGINQVIVFEETMAGPA
LQFTETPHLGRNQYIK

Signal sequence:

amino acids 1-27

Casein kinase II phosphorylation site.

amino acids 141-118, 253-257, 340-344, 395-399, 540-544, 560-564

N-myristoylation site.

amino acids 146-152, 236-242, 240-246, 244-250, 287-293, 309-315,
320-326, 366-372, 423-429, 425-431, 441-447, 503-509, 580-586

FIGURE 65

GGGGACGCGGAGCTGAGAGGCTCCGGGCTAGCTAGGTGTAGGGGTGGACGGGTCCCAGGACC
 CTGGTGAGGGTTCTCTACTTGGCCCTTCGGTGGGGGTCAAGACGACGGCACCTACGCCAAAGG
 GGAGCAAAGCCGGGCTCGGCCCGAGGCCCCAGGACCTCCATCTCCCAATGTTGGAGGAATC
 CGACACGTGACGGTCTGTCCGCGCTCTCAGACTAGAGGAGCGCTGTAAACGCCATGGCTCCC
 AAGAAGCTGTCTGCCTTCGTTCCCTGCTGCTGCCGCTCAGCCTGACGCTACTGCTGCCCCA
 GGCAGACACTCGGTCTGTTCTAGTGGATAGGGGTCTGACCGGTTTCTCCTAGACGGGGCCC
 CGTTCCGCTATGTGTCTGGCAGCCTGCACTACTTTCGGGTACCGGGGTGCTTTGGGCCGAC
 CGGCTTTGAAGATGCGATGGAGCGGCCTCAACGCCATACAGTTTATGTGCTCCCTGGAACATA
 CCACGAGCCACAGCCTGGGGTCTATAACTTTAATGGCAGCCGGGACCTTATTGGCTTTCTGA
 ATGAGGCAGCTCTAGCGAACCTGTGGTCATACTGAGACCGGACCTTACATCTGTGCAGAG
 TGGGAGATGGGGGTCTCCCATCTGGTTGCTTCGAAAACTGAAATTCATCTAAGAACCTC
 AGATCCAGACTTCTTGGCCGAGTGAATCTCGGTTCAAGGTCTTGTGCCCAAGATATATC
 CATGGCTTTATCACAATGGGGGCAACATCATTAGCACTCAGGTGGAGAAATGAATATGGTAGT
 TACAGAGCCTGTGACTTCAGCTCATGAGGCACCTGGCTGGGCTCTCCGTGCACTGCTAGG
 AGAAAAGATCTTGCTCTTACCACAGATGGGCGCTGAAGGACTCAAGTGTGGCTCCCTCCGGG
 GACTTATACACTGTAGATTTTGGGCCAGCTGACAACATGACCAAAATCTTTACCTGCTT
 CGGAAGTATGAACCCCATGGGCCATTGGTAAACTCTGAGTACTACAGGCTGGCGTGATTAT
 CTGGGGCCAGAATCACTCCACACGGTCTGTGTGAGCTGTAAACCAAGGACTAGAGAACATGC
 TCAAGTTGGGAGCCAGTGTGAACATGTACATGTTCCATGGAGGTACCAACTTTGGATATTGG
 AATGGTCCGATAGAAGGGACGCTTCCTCCGATTACTACCAGCTATGACTATGATGCACC
 TATATCTGAAGCAGGGGACCCACACCTAAGCTTTTGGCTCTTCGAGATGTCATCAGCAAGT
 TCCAGGAAGTTCTTTGGGACCTTTACCTCCCCGAGCCCCAAGATGATGCTTGGACCTGTG
 ACTCTGCACCTGGTTGGGCATTTACTGGCTTTCCTAGACTTGCTTTGGCCCCGTGGGCCCAT
 TCATTCAATCTTGCCAATGACCTTTGAGGCTGTCAAGCAGGACCATGGCTTCATGTTGTACC
 GAACCTATATGACCCATACCATTTTTGAGCCAAACCATTTCTGGGTGCCAAATAATGGAGTC
 CATGACCGTGCCATGTGATGGTGGATGGGGTGTCCAGGGTGTGTGGAGCGAAATATGAG
 AGACAAACTATTTTGCAGGGGAACTGGGGTCCAACTGGATATCTTGGTGGAGAACATGG
 GGAGGCTCAGCTTTGGGTCTAACAGCAGTGACTTCAAGGGCCTGTTGAAGCCACCAATTCTG
 GGGCAACAATCTCTACCCAGTGGATGATGTTCCCTCTGAAAATTGATAACCTTGTGAAGTG
 GTGGTTTCCCCCTCAGTTGCCAAAATGGCCATATCCTCAAGCTCCTTCTGGCCCCACATTCT
 ACTCCAAACATTTCCAATTTTAGGCTCAGTTGGGGACACATTTCTATATCTACCTGGATGG
 ACCAAGGGCCAAAGTCTGGATCAATGGGTTTAACTTGGGCCGGTACTGGACAAAGCAGGGGCC
 ACAACAGACCCCTCTACGTGCCAAGATTCTGCTGTTTCTAGGGGAGCCCTCAACAAAATTA
 CATTGCTGGAACTAGAAGATGTACCTCTCCAGCCCCAAGTCCAATTTTGGGATAAGCCCTATC
 CTCAAATAGCACTAGTACTTTGACAGGACACATATCAATTCCCTTTTCAGCTGATACACTGAG
 TGCCCTCTGAACCAATGGAGTTAAGTGGGCACTGAAAGGTAGGCCGGGCTATGTTGGCTCATGC
 CTGTAATCCAGCACATTTGGGAGGCTGAGACGGGTGGATTACCTGAGGTCAAGACTTCAAGA
 CCAGCCTGGCCAAATATGGTGAAACCCCGTCTCCACTAAAAATACAAAAATTAGCCGGGCGTG
 ATGGTGGGCACCTCTAATCCAGCTACTTGGGAGGCTGAGGGCAGGAGAATTGCTTGAATCC
 AGGAGGCAGAGGTTGCAGTGAGTGGAGGTGTACCACTGCATCCAGCCTGGCTGACAGTGA
 GACTCCATCTCAAAAAAAAAA

FIGURE 66

MAPKKLSCLRSLLLPLSLTLLLPQADTRSFVVDRGHRFLLDGAPFRYVSGSLHYFRVPRVL
WADRLKMRWSGLNAIQFYVPWNYHEPQPGVYNFNGSRDLIAFLNEAALANLLVILRPGPYI
CAEWEMGGLPSWLLRKPEIHLRTSDPDFLAAVDSWFKVLLPKIYPWLXHNNGNIISIQVENE
YGSYRACDFSVMRHLAAGLFRALLGEKILFTTDGPEGLKCGSLRGLYTTVDGFPADNMTKIF
TLRLKYEPHGPLVNSEYYTGWLDYWGQNHSTRSVSAVTKGLENMLKLGASVNMVMFHGGTNF
GYWNGADKKGRFLPITTSYDYDAPISEAGDPTPKLFALRDVISKFQEVPLGPLPPSPKMML
GPVTLHLVGHLLAFLDLLCPRGPIHSILPMTFEAVKQDHGFMLYRTYMTHTIFEPTPFWVFN
NGVHDRAYVMVDGVFQGVVERNMMDKFLFTGKLGSKLDILVENMGRLSFGSNSDDFKGLLKP
PILGQTILTQWMMFPLKIDNLVKWFFPLQLPKWPYPQAPSGPTFYSKTFPILGSGVGDTFLYL
PGWTKGQVWINGFNLGRYWTKQGPQQTLYVPRFLFPRGALNKITLLELEDVPLQPQVQFLD
KPILNSTSTLHRTHINSLSADTLSASEFMELSGH

Signal sequence:

amino acids 1-27

N-glycosylation site.

amino acids 97-101, 243-247, 276-280, 486-490, 625-629

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 4-8

Casein kinase II phosphorylation site.

amino acids 148-152, 234-238, 327-331, 423-427, 469-473, 550-554,
603-607, 644-648

Tyrosine kinase phosphorylation site.

amino acids 191-198

N-myristoylation site.

amino acids 131-137, 176-182, 188-194, 203-209, 223-229, 227-233,
231-237, 274-280, 296-300, 307-313, 447-453, 484-490

FIGURE 67

GCTTTGAACACGCTCTGCAAGCCCAAAGTTGAGCATCTGATTGGTTATGAGGTATTTGAGTGCA
ACCCACAATATGCGCTTACATGTTGAAAAAGCTTCTCATCAGTTACATATCCATTATTTGTGT
TTATGGCTTTATCTGCCTCTACACTCTCTTCTGGTTATTCTCAGGATACCTTTGAAGGAATATT
CTTTGAAAAAGTCAGAGAAGAGAGCAGTTTCTAGTGACATTCCAGATGTCAAAAACGATTTT
GCGTTCCTTCTTACATGGTAGACCAGTATGACCAGCTATATTCCAAGCGTTTGTGTGTGT
CTTGTGAGAAGTTAGTGAAAAATAAACTTAGGGAAATTAGTTTGAACCATGAGTGGACATTTG
AAAAACTCAGGCAGCACATTTACGCAACGCCAGGACAGCAGGAGTTGCATCTGTTTCATG
CTGTCGGGGGTGCCGATGCTGTCTTTGACCTCACAGACCTGGATGTGCTAAAGCTTGAAC
AATTCCAGAAGCTAAAAATCCTGCTAAGATTCTCAAATGACTAACCTCCAAGAGCTCCACC
TCTGCCACTGCCCTGCAAAAGTTGAACAGACTGCTTTTAGCTTTCTTCGCGATCACTTGAGA
TGCCCTTCACTGAAGTTCACTGATGTGGCTGAAATTCCTGCCTGGGTGTATTTGTCTCAAAAA
CCTTCGAGAGTTGTACTTAATAGGCAATTTGAACTCTGAAAACAATAAGATGATAGGACTTG
AATCTCTCCGAGAGTTGCGGCACCTTAAGATTCTCCACGTGAAGAGCAATTTGACCAAAGTT
CCCTCCAACATTACAGATGTGGCTCCACATCTTACAAAGTTAGTCATTATAATGACGGCAC
TAAACTCTTGGTACTGAACAGCCTTAAGAAAAATGATGAATGTGCTGAGCTGGAACCTCCAGA
ACTGTGAGCTAGAGAGAATCCACATGCTATTTTCAGCCTCTCTAATTTACAGGAACCTGGAT
TTAAAGTCCAATAACATTGCGACAATTGAGGAAATCATCAGTTTCCAGCATTAAAAACGACT
GACTTGTTTAAAAATTATGGCATAAATAAAATTGTTACTATTCTCCCTCTATTACCCATGTCA
AAAACCTTGAGTCACTTTATTTCTTAACAACAAGCTCGAATCCTTACCAGTGGCAGTATTT
AGTTTACAGAACTCAGATGCTTAGATGTGAGCTACAACAACATTTCAATGATTTCAATAGA
AATAGGATTGCTTCAGAACCTGCAGCATTTCATATCACTGGGAACAAGTGGACATTCTGC
CAAAACAATTTGTTTAAATGCATAAAGTTGAGGACTTTGAATCTGGGACAGAACTGCATCACC
TCACTCCAGAGAAAGTTGGTCACTCTCCAGCTCACTCAGCTGGAGCTGAAGGGGAACTG
CTTGACCGCTGCCAGCCAGCTGGGCCAGTGTGCGATGCTCAAGAAAAGCGGGCTTGTG
TGGAAGATCACCTTTTGATACCTGCCACTCGAAGTCAAAGAGGCATTGAATCAAGACATA
AATATTCCTTTGCAAAATGGGATTTAAACTAAGATAATATGCACAGTGATGTGCAGGAAC
AACTTCCTAGATTGCAAGTGCTCAGTACAAGTTATTACAAGATAATGCATTTTAGGAGTAG
ATACATCTTTTAAAAATAAACAGAGAGGATGCATAGAAGGCTGATAGAAGACATAACTGAAT
GTTCAATGTTTGTAGGGTTTAAAGTCATTATTTCCAAATCATTTTCTTTTCTTTTGGGG
AAAGGGAAGGAAAAATATAATCACTAATCTGGTTCCTTTTAAATGTTTTGTAACCTGGAT
GCTGCCGCTACTGAATGTTTACAAATGCTTGCCTGCTAAAGTAAATGATTAAATTGACATT
TTCTTACTAAAAA

FIGURE 68

MAYMLKKLLISYISIIICVYGFIGLYTLFWLFRIPPLKEYSFEKVVREESSFSDIPDVKNDFAPL
LHMVDQYDQLYSKRFGVFLSEVSENKLEISLNHEWTFEKLQKHISRNAQDKQELHLFMLS
VPDAVFDLTDLVDLKLLELIPEAKIPAKISQMTNLQELHLCHCPAKVEQTAFSFLRDHLRCLH
VKFTDVAEIPAWVYLLKNLRELYLIGNLSENKMKMIGLESRLRLHLKILHVKSNTLKVPSN
ITDVAPHLTKLVIHNDGTKLLVLNSLKKMMNVAELELQNCLELERIPHAIFSLSNLQELDLKS
NNIRTIEEIIISFQHLKRLTCLKLWHNKIVTIPPSITHVKNLESYFSSNNKLESPLVAVFSLQ
KLRLCDVSYNNISMPIEIGLLQNLQHLHITGNKVDILPKQLFKCIKRLTLNLGQNCITSLP
EKVGQLSQTQLELKGNCCLDRPLPAQLGQCRMLKKSGLVVEDHLFDTLPLEVKEALNQDINIP
FANGI

Signal sequence:

amino acids 1-20

N-glycosylation site.

amino acids 241-245, 248-252, 383-387

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 326-330

Casein kinase II phosphorylation site.

amino acids 48-52, 133-137, 226-230, 315-319, 432-436, 444-448

Tyrosine kinase phosphorylation site.

amino acids 349-355, 375-381

N-myristoylation site.

amino acids 78-84, 124-130, 212-218, 392-398

FIGURE 69

CCCACGCGTCCGGCCCTTCTCTGGACTTGCATTTCATTCTTTTCATTGACAACTGACITTTTTTTTATTCTT
 TTTTTTTCATCTCTGGGCCAGCTTGGGATCTTAGGCCGCCCTGGGAAGACATTTGTGTTTTACACACATAAGGAT
 CTGTGTTTGGGGTTTCTCTCTCCCTGCACATTGGCATTGCTTGTGTGTGTGTGGGGAGGAGACCAAGCTGG
 GCTCAGTGCCTGCTTGACTTATCTGCCTTAGGTACATCGAAGTCTTTTGACCTCCATACAGTGATTTATGCTGTCT
 ATCGCTGTGTGATCTGAGGCGCCCTTGTCTCTGCTGATAGTTGTGTGTCTGTCTTTTACTTCAAAATACACAAC
 AACAGCCAGGSCAAAACCATTTGCCACGGAGTCTTGTCTCTGCCCTGCAGTGTGTGAAGGATATAGAATGTGTGCC
 AGTTTTTGATTTCCCTGCCACCTTGTCTGTGCGACATAAATGAGGCGCTCTGAGTTAGGAAAGGCTCCCTTCTCAAA
 GCAGAGCCCTGAAGACTTCAATGATGTCAATGAGGCCACCTGTTTGTGATGTGCAGGCCACAGAAGAAAGGCACAG
 CTCGCCATCAGTTTTCATGGAATAAATCAGTGCCTCTGCGGAACAGCTGTGTGAGATCCCTACAGAGAGCTTCT
 CACTGGGGCAACCCCTCCAGGAAGGAGTTGGGGAGAGAGAACCCTCACTGTGGGGAATGCTGATAAACCCAGTCA
 CACAGCTGCTCTATTCTCACACAAATCTACCCCTTGCCTGCTGGAAGTGTCCCTGGAGGTGTCCAGAAA
 GCTGATGTAACACAGAGCCTATAAAAGCTGTCGGTCTTAAAGCTGCCAGCGCTTGCCTGAGAGCTTGTGTA
 AGAAGGCTCATGCCATTGACCCCTTAAATCTCTCTCTGCTTGTGGCGGAGCTGACCAATGGCGGAGGCTGAAGGCAAT
 GCAAGCTGCACAGTCACTTAGGGGGTGCCAAATATGCGAGAGACCCACAAAGCCATGATCCTGCAACTCAATCCC
 AGTGAGAACTGCACCTGGACAAATAGAAAGACAGAAAACAAAGCATCAGAATTTATCTTTTCTATGTCCAGCTT
 GATCCAGATGGAAGCTGTGAAGGTGAAACATTAAGTCTTTGACGGAACCTCCAGCAATGGGCCCTCTGCTAGGG
 CAGTCTCGAGTAAAAACGACTATGTTCTGTATTTGAATCATCATCCAGTACATTGACGTTTCAAATAGTTAGT
 GACTCAGCAAGAATCAAAGAACTGTCTTTGTCTTCTACTACTTCTCTCTCCTAACATCTCTATTCCAAACTGT
 GCGGTTTACCTGGATACCTTGGAGGATCCTTACCAGCCCAATTACCCAAAGCCGATCCTGAGCTGGCTTAT
 TGTGTGTGGCACATACAAGTGGAGAAAGATTACAAGATAAACTAAACTTCAAAGAGATTTTCTAGAAATAGAC
 AAACAGTCAAAATTTGATTTTCTGCAATCTATGATGGCCCCCTCCACCAACTCTGGCCTGTGGACAAAGTCTGT
 GGCCTGTGATCTCCACCTTCGAATCGTCATCAAATCTCTGACTGTGTGTGTGTCTCAGATTATGCCAACTGT
 TACCGGGGATTTTCTGCTTCTTACACCTCAATTTATGACGAAAACATCAACACTACATCTTTAACTTGTCTCTCT
 GACAGGATGAGAGTTATTAATAGAACCTTCACTTAGAGGCTTTTAACTCTAATGGGAATAACTGCACTAAAA
 GACCCAACTTGACAGACAAAATATCAAATGTGTGGAATTTTCTGTCTCTTAAATGGATGTGGTACAACTCAGA
 AAGGTAGAAGATCAGTCAATTTATACACCAATATAATCACTTTTCTGCATCTTCAAGCTTGAAGTATCACC
 CGTCAGAAACAACTCCAGATTTATGTGAAGTGTGAATGGGACATAATTTACAGTGGAGATAATATACATAACA
 GAAGATGATGTAATACAAAGTCAAAATGCATCGGGCAAAATATAACACAGCATGGCTCTTTTTGTAATCCAAATCA
 TTTGAAAAGACTATACTGAAATCACCATAATATGTGGATTTGAACCAAAGCTTTTTTGTTCAGGTAGTCTGCAC
 AACTCAGATCCAAATTTGGTGGTGTTCCTGATACCTGTAGAGCCTCTCCACCTCTGACTTTGCACTTCCACCC
 TACGACCTTAATCAAGAGTGGATGTAGTCGAGATGAAACTGTGAAGGTGATCCCTTATTTGGACACTATGGGAGA
 TTTCCAGTTTAAATGCTTTAAATCTTGGAGAAGTATGAGCTCTGTGTATCTGCAAGTGTAAAGTTTGTATATGTAT
 AGCAGTGACCACCAAGCTCTGCTGCAATCAAGGTTGTGTCTCCAGAAACAAACGAGACATTTCTCATATAAATGG
 AAAACAGATTCATCATAGGACCCATTCGCTGAAAAGGGATCGAAGTGCAGTGGCAATTCAGGATTTTCAGCAT
 GAAACACATGCGGAAGAACTCCAAACAGCCCTTCAACAGTGTGCATCTGTTTCTCTTCAATGAGTCTGAGCTG
 AATGTGTGATCTGAGCACAATCAGTGAAGGCATTTTGAATTAACAGGGCAGACTACAAATACCAAGAGCTG
 CAGAATCTTAACAAAGGTCACCCCTAAGTGAGACATGTTCTCCAGGATGCAAAGGAAATGCTACCTCGT
 GGCTACACATATTATGAATAAATGAGGAAGGCCCTGAAAGTGACACACAGGCCCTGCATGTAAAAAAA

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FIGURE 70

MELVRRLMPLTLLILSCLAELTMAEAEGNASCTVSLGGANMAETHKAMILQLNPSENCTWTI
ERPENKSIRIIIFSIVQLDPDGSCESENIKVFDGTSSNGPLLGGVCSKNDYVVPVFESSSSLT
FQIVTDSARIQRTVFVFYFFSPNISIPNCGGYLDTLEGSFTSPNYPKHPPELAYCVWHIQV
EKDYKIKLNFKEIFLEIDKQCKFDFLAIYDGPSTNSGLIGQVCGRVTPTFESSSNSLTVVLS
TDYANSYRGFSASYTSIYAENINTTSLTCSSDRMRVLIISKSYLEAFNSNGNQLKDPTCRP
KLSNVVEFSVPLNGCGTIRKVEDQSITYTNIITFSASSTSEVITRQKQLQIIVKCEMGNST
VEIIYITEDDDVIQSQUALGKYNTSMALFESNSFEKTILESPYYVDLNQTLFVQVSLHTSDPN
LVVFLDTCRASPTSDFASPTYDLIKSGCSRDETCKVYPLFGHYGRFQFNAFKFLRSMSSVYL
QCKVLICDSSDHQSRCNQCVSRSKRDISSYKWKTDSSIIGPIRLKRDRSASGNSGFQHETHA
EETPNQPFNSVHLFSFMVLALNVVTVATITVRHFVNQRADYKYQKLQNY

Signal sequence:

amino acids 1-24

Transmembrane domain:

amino acids 571-586

N-glycosylation site.

amino acids 29-33, 57-61, 67-71, 148-152, 271-275, 370-374,
394-398, 419-423

Casein kinase II phosphorylation site.

amino acids 22-26, 108-112, 289-293, 348-352, 371-375, 379-383,
408-412, 463-467, 520-524, 556-560

Tyrosine kinase phosphorylation site.

amino acids 172-180, 407-415, 407-416, 519-528

N-myristoylation site.

amino acids 28-34, 38-44, 83-89, 95-101, 104-110, 226-232

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

FIGURE 71

GACGGAAGAACAGCGCTCCCGAGGCGCGGGAGCCTGCAGAGAGGACAGCCGGCCTGCGCCG
GGACATGCGGCCCCAGGAGCTCCCGAGGCTCGCGTTCCCGTGTGCTGTTGCTGCTG
TGCTGCCCGCCGCCGCGTGCCTGCCACAGCGCCACGCGCTTCGACCCCACTGGGAGTCC
CTGGACGCCCGCAGCTGCCCGCGTGGTTTGACCAGGCCAAGTTCGGCATCTTCATCCACTG
GGGAGTGTTTTTCCGTGCCAGCTTCGGTAGCGAGTGGTTCTGGTGGTATTGGCAAAAGGAAA
AGATACCGGAAGTATGTGGAATTTATGAAAGATAATTACCTCCCTAGTTTCAAATATGAAGAT
TTTGGACCACTATTTACAGCAAAATTTTTTAATGCCAACAGTGGGCAGATATTTTTTCAGGC
CTCTGGTGCCAAATACATTGTCTTAACCTCCAAACATCATGAAGGCTTTACCTTGTGGGGGT
CAGAATATTCTGGGAAGTGGAAATGCCATAGATGAGGGGCCCAAGAGGGACATTTGTCAAGGAA
CTTGAGGTAGCCATTAGGAACAGAACTGACCTGCGTTTTGGACTGTACTATTCCCTTTTTGA
ATGTTTTATCCGCTCTTCCCTTGAGGATGAATCCAGTTTCATTCCATAAGCGGCAATTTCCAG
TTTCTAAGACATTGCCAGAGCTCTATGAGTTAGTGAACAACATATCAGCCTGAGGTTCTGTGG
TCGGATGCTGACGGAGGAGCACCGGATCAATACTGGAACAGCACAGGCTTCTTGGCCTGGTT
ATATAATGAAAGCCCGATTCGGGGGCACAGTAGTCACCAATGATCGTTGGGGAGCTGGTAGCA
TCTGTAAGCATGGTGGCTTCTATACCTGCAGTGATCGTTATAACCCAGGACATCTTTTGCCA
CATAAATGGGAAAACATGCATGACAATAGACAAACTGTCTGGGGCTATAGGAGGGGAAGCTGG
AATCTCTGACTATCTTACAATTGAAGAATTGGTGAAGCAACTTGTAGAGACAGTTTTCATGTG
GAGGAAATCTTTTGATGAATATTGGGCCCACTAGATGGCACCATTCTGTAGTTTTTGTAG
GAGCGACTGTAGGCAAGTGGGGTCTGGCTAAAAGTCAATGGAGAAGCTATTTATGAAAACCTA
TACCTGGCGATCCAGAAATGACACTGTCAACCCAGATGTGTGGTACACATCCAAGCCTAAAG
AAAAATTAGTCTATGCCATTTTTCTTAAATGGCCACATCAGGACAGCTGTTCTCTTGGCCAT
CCCAAAGCTATTCTGGGGGCACAGAGGTGAAACTACTGGGCCATGGACAGGCCACTTAACTG
GATTTCTTTGGAGCAAAATGGCATTATGGTAGAACTGCCACAGCTAACCAATTCATCAGATGC
CGTGTAATGGGGCTGGGCTCTAGCCCTAACTAATGTGATCTAAAGTGCAGCAGAGTGGCTG
ATGCTGCAAGTTATGTCTAAGGCTAGGAACTATCAGGTGTCTATAAATTGTAGCACATGGAGA
AAGCAATGTAAACTGGATAAGAAAATTTATTTGGCAGTTCAGCCCTTTCCCTTTTTCCCACTA
AATTTTTCTTAAATTACCATGTAAACATTTTAACTCTCCAGTGCATTTGGCATTAAAGTC
TCTTCACATTGATTGTGTTCCATGTGTGACTCAGAGGTGAGAATTTTTTTCACATTATAGTAG
CAAGGAATTGGTGGTATTATGGACCGAACTGAAAATTTTATGTTGAAGCCATATCCCCATG
ATTATATAGTTATGCATCACTTAATATGGGGATATTTCTGGGAAATGCATTGCTAGTCAAT
TTTTTTTTGTGCCAATCATAGAGTGTATTACAAAATCCTAGATGGCATAGCCTACTACA
CACCTAATGTGTATGGTATAGACTGTTGCTCCTAGGCTACAGACATATACAGCATGTTACTG
AATACTGTAGGCAATAGTAACAGTGGTATTTGTATATCGAAACATATGGAACATAGAGAAG
GTACAGTAAAAAATACTGTAAAATAAATGGTGACCTGTATAGGGCACTTACCACGAAATGGAG
CTTACAGGACTGGAAGTTGCTCTGGGTGAGTGCAGTGAGTGAAGTGTGAAGGCTTAGGACATT
TTGAACACTGCCAGACGTTATAAATACTGTATGCTTAGGCTACACTACATTTATAAAAAAAA
GTTTTTCTTCTTCAATTATAAATTAACATAAGTGTACTGTAACTTTACAACGTTTTAATT
TTTAAACCTTTTTTGCGCTTTTTGTAATAACACTTAGCTTAAAAACATAAATCATTTGTGCAA
ATGTAA

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FIGURE 72

MRPQELPRLAFLPLLLLLLLLLPPPPCPAHSATRFDPWTWESLDARQLPAWFDQAKFGIFIHWG
VFSVPSPFGSEWFWWYQKEKIPKYVEFMKDNYPSPFKYEDFGPLFTAKFFNANQWADIFQAS
GAKYIVLTSKHHEGFTLWGSEYSWNWNAIDEGPKRDIVKELEVAIRNRTDLRFGLYYSLEW
FHLPLFLEDESSFHKRQFPVSKTLPELYELVNNYQPEVLWSDGDGGAPDQYWNSTGFLAWLY
NESPVRGTVVTNDRWGAGSICKHGGFYTCSDRYNPGHLLPHKWENCMTIDKLSWGYRREAGI
SDYLTIEELVKQLVETVSCGNLLMNIGPTLDGTISVVFEERLRQVGSWLKVNGEAIYETYT
WRSQNDTVTPDVWYTSKPKKEKLVAIFLKWPTSGQLFLGHFKAILGATEVKLLGHGQPLNWI
SLEQNGIMVELPQLTIHQMPCKWGWALALTNVI

Signal sequence:

amino acids 1-28

N-glycosylation site.

amino acids 171-175, 239-243, 377-381

Casein kinase II phosphorylation site.

amino acids 32-36, 182-186, 209-213, 227-231, 276-280, 315-319,
375-375

Tyrosine kinase phosphorylation site.

amino acids 361-369, 389-397

N-myristoylation site.

amino acids 143-149, 178-184, 255-261, 272-278, 428-434

Leucine zipper pattern.

amino acids 410-432

Alpha-L-fucosidase putative active site.

amino acids 283-295

FIGURE 73

AGCAGGGAAATCCGGATGTCTCGGTTATGAAGTGGAGCAGTGAGTGTGAGCCTCAACATAGT
TCCGAAACTCTCCATCCGGACTAGTTATTGAGCATCTGCCTCTCATATCACCAGTGGCCATC
TGAGGTGTTTCCCTGGCTCTGAAGGGGTAGGCACGATGGCCAGGTGCTTCAGCCTGGTGTG
CTTCTCACTTCCATCTGGACCACGAGGCTCTCTGGTCCAAGGCTCTTTGCGTGCGAAGAGCT
TTCCATCCAGGTGTCTGTCAGAAATTATGGGGATCACCTTGTGAGCAAAAAGGCGAACACAGC
AGCTGAATTTTCAGAGAAGCTAAGGAGGCCTGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAG
GACCAAGTTGAAACAGCCTTGAAGCTAGCTTTGAAACTTGCAGCTATGGCTGGGTGGAGA
TGGATTGCTGGTCACTCTCTAGGATTAGCCAAACCCCAAGTGTGGGAAAAATGGGGTGGGTG
TCCTGATTTGGAAGGTTCCAGTGAAGCCGACAGTTTGCAGCCTATTGTTACAACCTCATCTGAT
ACTTGGACTAACTCGTGCATTCCAGAAATTATCACCACCAAGATCCCATATTTCAACACTCA
AACTGCAACACAAACACAGAATTTATTGTGTCAGTGACAGTACCTACTCGGTGGCATCCCTT
ACTCTACAATACCTGCCCTACTACTACTCTCTCTGCTCCAGCTTCCACTTCTATTCCACGG
AGAAAAAATTGATTTGTGTACAGAAGTTTATTGGAAGTATAGCACCATTGTCTACAGAAAC
TGAACCATTTTGTGAAAATAAAGCAGCATTCAGAATGAAGCTGCTGGGTTTGGAGGTGTCC
CCACGGCTCTGCTAGTGTCTGCTCTCTCTCTTCTTTGGTGTCTGCAGCTGGTCTTGGATTTGTC
TATGTCAAAGGTATGTGAAGGCCTTCCCTTTTACAAACAAGAATCAGCAGAAGGAAATGAT
CGAAACCAAAGTAGTAAAGGAGGAGAAGGCCAATGATAGCAACCCCTAATGAGGAATCAAAGA
AAACTGTAAAAAACCCAGAGAGTCCAAGAGTCCAAGCAAAACTACCGTGCAGTGCCTGGAA
GCTGAAGTTTAGATGAGACAGAAATGAGGAGACACACCTGAGGCTGGTTTCTTTCATGCTCC
TTACCCTGCCCCAGCTGGGGAATCAAAGGGCCAAAGAACCAAGAAGAAAGTCCACCTT
GGTTCCTAAGTGAATCAGCTCAGGACTGCCATTGGAATATGGAGTGACACAAAGAGAATGC
CCTTCTCCTTATTGTAACCTGTCTGGATCCTATCCTCCTACCTCCAAAGCTTCCCACGGCC
TTTCTAGCCTGGCTATGTCTTAATAATATCCCACTGGGAGAAAGGAGTTTTCGAAAGTGCAA
GGACCTAAACATCTCATCAGTATCCAGTGGTAAAAAGGCCCTCTGGCTGTCTGAGGCTAGG
TGGGTTGAAAGCCAAGGAGTCACTGAGACCAAGGCTTCTCTACTGATTCGCGAGCTCAGAC
CCTTCTCTCAGCTCTGAAGAGAAACACGTATCCCACCTGACATGTCTTCTGAGCCCGGTA
AGAGCAAAAGAAATGGCAGAAAAGTTTAGCCCTGAAAGCCATGGAGATTCTCATAAATTGAG
ACCTAATCTCTGTAAGCTAAATAAAGAAATAGAACCAAGGCTGAGGATACGACAGTACACT
GTCAGCAGGACTGTAAACACAGACAGGCTCAAAGTGTCTTCTCTGAACACATTGAGTTGGA
ATCACTGTTTAGAACACACACACTTACTTTTTCTGGTCTCTACCACTGCTGATATTTTCTCT
AGGAAATATACTTTTACAAGTAACAAAAATAAAACTCTTATAAATTCTATTTTATCTGTA
GTTACAGAAATGATTACTAAGGAAGATTACTCAGTAATTTGTTTAAAAAGTAATAAAATTCA
ACAAACATTTGCTGAATAGCTACTATATGTCAAGTGCTGTGCAAGGTATTACACTCTGTAAT
TGAATATTATCTCAAAAAATTGCACATAGTAGAACGCTATCTGGGAAGCTATTTTTTCA
GTTTGTATTTCTAGCTTATCTACTTCCAAACTAATTTTTTGTGCTGAGACTAATCTT
ATTCAATTTCTCTAATTTGGCAACCATTATAACCTTAATTTATTATTAAACATACCTAAGAAG
TACATTTGTTAACTCTATATACAAAGCACATTTTAAAGTGCCATTAAACAAATGTATCATA
GCCCTCCTTTTTCCAACAAGAGGGACTGAGAGATGCAGAAATATTGTGACAAAAAATTA
AGCATTAGAAAACTT

0998572:074004

FIGURE 74

MARCFSLVLLLTISIWTTRLLVQGSRLAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACR
LLGLSLAGKDQVETALKASFETCSYGWVGDFVVISRISPNPKCGKNGVGLIWKVPVSRQF
AAYCYNSSDTWTNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTPP
APASTSIPRRKKLICVTEVFMETSTMSTETEPFVENKAAFNEAGFGGVPTALLVLALLFF
GAAAGLGCYCVKRYVKAFPTNKNQQKEMIETKVVKEEKANDSNPNEEKKTDKNPEESKSP
SKTTVRCLEAEV

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 235-254

N-glycosylation site.

amino acids 53-57, 130-134, 289-293

Casein kinase II phosphorylation site.

amino acids 145-149, 214-218

Tyrosine kinase phosphorylation site.

amino acids 79-88

N-myristoylation site.

amino acids 23-29, 65-71, 234-240, 235-239, 249-255, 253-259

FIGURE 75

AGATGGCGGTCTTGGCACCTCTAATTGCTCTCGTGATTTCGGTGCCGCGACTTTCACGATGG
CTCGCCCAACCTTACTACCTTCTGTGCGCCCTGCTCTCTGCTGCCTTCTACTCTGAGGAA
ACTGCGCGCGCTCTGCCACGCTCTGCCACCCAACGCAAGACGGTAACCCGTGTGACTTTG
ACTGGAGAGAAGTGGAGATCTGTATGTTTCTCAGTGCCATTGTGTATGATGAAGAACCGCAGA
TCCATCACTGTGGAGCAACATATAGGCAACATTTTCATGTTTAGTAAAGTGGCCAACACAAT
TCTTTTCTCCGCTTGGATATTGCGATGGGCCTACTTTACATCACACTCTGCATAGTGTTC
TGATGACGTGCAAAACCCCCCTATATATGGGCCCTGAGTATATCAAGTACTTCAATGATAAA
ACCATTGATGAGGAACTAGAACGGGACAAGAGGGTCACTTGGATTGTGGAGTTCCTTGGCAA
TTGGTCTAATGACTGCCAATCATTTGCCCTATCTATGCTGACCTCTCCCTTAAATACAAC
GTACAGGGCTAAATTTTGGGAAGGTGGATGTTGGACGCTATACTGATGTTAGTACGCGGTAC
GAAGTGAGCACATCACCCCTCACCAAGCAACTCCCTACCCGTGATCTGTTCGAAGGTGGCAA
GGAGGCAATGCGGCGGCCACAGATTGACAAGAAAGGACGGGCTGTCTCATGGACCTTCTCTG
AGGAGAATGTGATCCGAGAATTTAACTTAAATGAGCTATACCAGCGGGCCAAGAAACTATCA
AAGGCTGGAGACAATATCCCTGAGGAGCAGCCTGTGGCTTCAACCCCCCAACAGTGTGAGA
TGGGGAAAAACAAGAAGGATAAATAAGATCCTCACTTTGGCAGTGCTTCTCTCTGTCAATT
CCAGGCTCTTCCATAAACCAAGCCTGAGGCTGCAGCCTTTNATTNATGTTTTCCTTTGG
CTGNGACTGGNTGGGCAGCATGCAGCTTCTGATTTTAAAGAGGCATCTAGGGAATTGTGAG
GCACCTTACAGGAAGGCCTGCCATGCTGTGGCCAAGTCTTCACTGGAGCAAGAAAGAGATC
TCATAGGACGGAGGGGGAATGTTTCCCTCCAAGCTTGGGTCAAGTGTGTTAACTGCTTATC
AGCTATTTCAGACATCTCCATGGTTTCTCCATGAACTCTGTGGTTTCATCATTCTCTTAG
TTGACCTGCACAGCTTGGTTAGACCTAGATTAAACCCTAAGGTAAGATGCTGGGGTATAGAA
CGCTAAGAAATTTCCCCCAAGGACTCTTGCTTCCCTAAGCCCTTCTGGCTTCGTTTATGGTC
TTCATTAAGTATAAGCCCTAACTTTGTGCTAGTCTAAGGAGAAACCTTTAACCACAAAG
TTTTTATCATTTGAAGACAATATTGAACAACCCCTATTTTGTGGGATTGAGAAGGGGTGAA
TAGAGGCTTGAGACTTTCCTTTGTGTGGTAGGACTTGGAGGAGAAATCCCCTGGACTTTCAC
TAACCCCTTGACATACTCCCCACACCCAGTTGATGGCTTTCGTAATAAAAAAGATTGGGATT
TCCTTTTG

FIGURE 76

MAVLAPLIALVYSVPRLSRWLAQPYLLSALLSAAFLLVRLPPLCHGLPTQREDGNPCDFD
WREVEILMFLSAIVMMKNRRSITVEQHIGNIFMFSKVANTILFFRLDIRMGLLYITLCIVFL
MTCKPPLYMGPEYIKYFNDKTIDEELERDKRVTWIVEFFANWSNDCQSFAPIYADLSLKYNC
TGLNFGKVDVGRYTDVSTRYKVSTSP LTKQLPTLILFQGGKEAMRRPQIDKKGRAVSWTFSE
ENVIREFNLNELYQRAKKLSKAGDNIPEEQPVASTPTTVSDGENKKDK

Signal sequence:

amino acids 1-48

Transmembrane domain:

amino acids 111-125

N-glycosylation site.

amino acids 165-169, 185-189

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 154-158, 265-269

Casein kinase II phosphorylation site.

amino acids 51-55, 145-149, 245-249, 286-290, 288-292

N-myristoylation site.

amino acids 188-194, 225-231

Myb DNA-binding domain repeat signature 1.

amino acids 244-253

0902572-071004

[illegible]

FIGURE 78

MGLLLLPLLLLPGSYGLPFYNGFYYSNSANDQNLGNHGKDLLNGVKLVVETPEETLFTYQ
GASVILPCRYYEPALVSPRRVRVKWWKLSENGAPEKDVLVAIGLRHRSFGDYQGRVHLRQD
KEHDVSLEIQDLRLDYGRYRCEVIDGLEDESGLVELELRGVVFPYQSPNGRYQFNFHEGQQ
VCAEQAAVVASFQELFRWEEGLDWCNAGWLQDATVQYPIMLPQPCGGPGLAPGVRSYGPR
HRRLLHRYDVFCFATALKGRVYYLEHPEKLTLTAREACQEDDATIAKVGQLFAAWKFHGLDR
CDAGWLADGSVRYPPVHHPNCGPPEPGVRSFGFPDPQSRLYGVYCYRQH

Signal sequence:

amino acids 1-17

Casein kinase II phosphorylation site.

amino acids 29-33, 53-57, 111-115, 278-282

Tyrosine kinase phosphorylation site.

amino acids 137-145

N-myristoylation site.

amino acids 36-42, 184-190, 208-214, 237-243, 297-303, 307-313

FIGURE 79

GGAGAGCGGAGCGAAGCTGGATAACAGGGGACCG**ATG**ATGTGGCGACCATCAGTTCTGCTGC
TTCTGTTGCTACTGAGGCACGGGGCCAGGGGAAGCCATCCCCAGACGCAGGCCCTCATGGC
CAGGGGAGGGTGCACCAGGCGGGCCCCCTGAGCGACGCTCCCCATGATGACGCCCACGGGAA
CTTCCAGTACGACCATGAGGCTTTCTGGGACGGGAAGTGGCCAAGGAATTCGACCAACTCA
CCCCAGAGGAAAGCCAGGCCCCGTCTGGGGCGGATCGTGGACCGCATGGACCGCGCGGGGGAC
GGCGACGGCTGGGTGTCTGCTGGCCGAGCTTCGCGCGTGGATCGCGCACACGCAGCAGCGGCA
CATACGGGACTCGGTGAGCGCGGCCTGGGACACGTACGACACGGACCGCGACGGGCGTGTGG
GTTGGGAGGAGCTGCGCAACGCCACCTATGGCCACTACGCGCCCCGTGAAGAATTTTCATGAC
GTGGAGGATGCAGAGACCTACAAAAAGATGTGGCTCGGGACGAGCGCGCTTTCGGGTGGC
CGACCAGGATGGGGACTCGATGGCCACTCGAGAGGAGCTGACAGCCTTCTCGCACCCCGAGG
AGTTCCCTCACATGCGGGACATCGTGATTGCTGAAACCTTGGAGGACCTGGACAGAAACAAA
GATGGCTATGTCCAGGTGGAGGAGTACATCGCGGATCTGTACTCAGCCGAGCCTGGGGAGGA
GGAGCCGGCGTGGGTGCAGACGGAGAGGCAGCAGTTCCGGGACTTCCGGGATCTGAACAAGG
ATGGGCACCTGGATGGGAGTGAGGTGGGCCACTGGGTGCTGCCCCCTGCCAGGACCCAGCCC
CTGGTGGAAGCCAACCACCTGCTGCACGAGAGCGACACGGACAAGGATGGGCGGCTGAGCAA
AGCGGAAATCTGGGTAATTGGAACATGTTTGTGGGCAGTCAGGCCACCAACTATGGCGAGG
ACCTGACCCGGCACCACGATGAGCTG**TG**AGCACCGCGCACCTGCCACAGCCTCAGAGGCCG
CACAATGACCGAGGAGGGGGCCGCTGTGGTCTGGCCCCCTCCCTGTCCAGGCCCCGAGGAG
GCAGATGCAGTCCAGGCATCTCTGCCCCCTGGGCTCTCAGGAGCCCCCTGGGTGCGCTTC
TGTCCCTGTACACCCCCAACCCAGGGAGGGGCTGTATAGTCCAGAGGATAAGCAATAC
CTATTTCTGACTGAGTCTCCAGCCAGACCCAGGGACCTTGGCCCCAAGCTCAGCTCTAA
GAACCGCCCCAACCCCTCCAGCTCCAAATCTGAGCCTCCACCACATAGACTGAAACTTCCCT
GGCCCCAGCCCTCTCTGCTGGCTGGCCTGGGACACCTCCTCTCTGCCAGGAGGCAATAA
AAGCCAGCGCCGGGACCTTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAA

FIGURE 80

MMWRPSVLLLLLLLRHGAQ GKPS PDAGPHGQGRVHQAAPLSDAPHDDAHGNFQYDHEAFLGR
EVAKEFDQLTP EESQARLGRIVDRMDRAGDGDGWVSLAELRAWIAHTQQRHIRDSVSAAWDT
YDTRDRDGRVGWEELRNATYGHYAPGEEFHDVEDAET YKKMLARDERRFRVADQDGD SMATRE
ELTAFLHP EEFPHMRDIVIAETLEDLDRNKDGYVQVEEYIADLYSAEPGEEEP AWVQTERQQ
FRDFRDLNKDGHLDGSEVGHWVLP AQDQPLVEANHLLHESDTDKDGRLSKAEILGNWNMFV
GSQATNYGEDLTRHHDEL

Signal sequence:

amino acids 1-20

N-glycosylation site.

amino acids 140-144

Casein kinase II phosphorylation site.

amino acids 72-76, 98-102, 127-131, 184-188, 208-212, 289-293,
291-295, 298-302

N-myristoylation site.

amino acids 263-269, 311-317

Endoplasmic reticulum targeting sequence.

amino acids 325-330

03200757 074001

GGGGCCTTGCCTTCCGCACTCGGGCGCAGCCGGGTGGATCTCGAGCAGGTGCGGAGCCCCGG
GCGGCGGGCGCGGGTGCAGAGGATCCCTGACGCCTCTGTCTCCTTGTCTTTGTGCGTCCGAC
CTCTGTCTGTCTCGTTTGTGCGCCGCCGCTCCCGCGGTGCGGGTGTGCACACCATCTGTG
GGCTTCGCTCGATTGTGCGCGCAGAGCGCTCCGACACTGAGAGGGCGCTTGCCTTGAGCAG
CGGGTCTGTGTCCTCTCTCTCTGCTGCGCCGCCGGGGATCCGAGGGGTGCGGGGCTCT
GAGGAGGTGACGCGCGGGGCTCCGCGACCTTGGCCTTGGCCGATCTCCCTCTCTCCGAC
GTGTGAGCAGCCTATCAGTCCACATGTGCGCCGACCTGGATTCGCGGCTCTCGGCCTCGGTGT
TGTCGTCTGCTGCTCGCGGGCCCGGGGACGAGGAGGAGCCCTCCATTGCTATCATAT
TTTACAGAGGCTTGGACATCAGGAAAGAGAAAGCAGATGTCTCTGCCAGGGGGCTGCC
CTCTTGAAGGAATTTCTGTGTATGGGAACTAGTATATGCTTGTATCGAGCATATGTGGG
GCTGCTGTCCACAGGGGAGTAATCAGCAACTCAGGGGGACCTGTACAGACTATAGCTTACG
TGCTCGAGAAAACTATTCTCAGTAGATGCCAAATGGCATTCAGTCTCAAATGCTTTCTAGAT
GGTCTGCTTCTTTCAGATAACTAAAGCAAAGTAGTACACAGGAGGCCACAGGACAAGCA
GTGTCCACAGCACATCCACCACAGGTAAACGACTAAAGAAAACACCCGAGAAGAAACTGG
CAATAAAGATTTGTAAGCAGACATTGCTTGTGTGATTTGATGGAAGCTTTAATATTTGGCGAGC
CGCGATTTAAATTTACAGAAGAAATTTGTTGGAAAGATGGCTCTAATGTGGGAATTTGAAACA
GAAGGACACATGTGGGCTTGTTCAGGCGAGTGAACATCCCAAATTAAGAATTTTACTTGAA
AAACTTTACATCAGCCAAAGATGTTTGTGTTGCCATAAAGGAATAGGTTTACAGAGGGGTA
ATTCCCAATACAGGAAAAGCTTTGAAGCATATGCTCAGAAATTTCTACCGTAGATGCTGGA
GTAAGAAAAGGATCCCCAAAGTGTGGTGGTATTTATTTGATGTTTGGCCTTCTGATGACAT
CAGGAAGACAGGCATTTGGGCCAGAGAGTTTGGTGTCAATGTATTTATAGTTTCTGTGGCCA
AGCCTATCCTCGAAGAACTGGGGATGGTTCAGGATGTACATTTGTTGACAAGGCTGTCTGT
CGGAATAATGGCTTCTTCTTACCATCAGCCAACTGGTTTGGCACACAAAATACGTAA
GCCTCTGGTACAGAAGCTGTGCATCATGAACAAATGATGTGCAGCAAGACTGTTATAACT
CAGTGAACATTTGCCCTTCTAATTTGATGGCTCCAGCAGTGTGGAGATAGCAATTTCCGCGCTC
ATGCTTGAAATTTGTTTCCCAACTGACCAAGACTTTGAAATCTCGCAAGTGTGGTGCCAAGAT
AGCTCGTGTACAGTCTTACTATGATCAGCGCACGGAGTTTCAGTTTCACTGACTATAGCACC
AAGAAGATGCTCAGTGTCTATCAGAAACATCCGCTATATAGTGTGGAAACGACTAGGT
GATGCCATTTCTTCACTGTTAGAAATGTGTTTGGCCCTATAGGAGGAGCCCAACAGAA
CTTCTAGTAATTTGTACAGATGGGCGCTTATGATGATGTGCACAGGCGCTGACGCTGCTG
CATGTATCGGAATCATCATCTCTCTCTGTTGGTGTGGCTTGGGCACCTCTGATGACTGT
AAGATGATGGCTTCTAAGACGAAGGATCTCACGCTTCTTTCACAAGAGAGTTACAGGATT
AGAACCAATGTTTGTGATGTCTCAGAGGCATTTGATAGATTCTTAGAATCCCGACAAT
AATGGTAACTATTGACAATGTAAGAAAAAGTACAGGGGATCAGTGTGTAATTTGATT
CTCATAATCTGAAGTCTTTAGCATATAGATACAGATACAAAATTAAGTATGTCAAC
AGCCATTTAGGCAAAATAGCACTCCTTAAAGCGCTGCTTCTGTTTACAATTTACAGTGT
ACTTGTGTTAAAAACACTGTCTGAGGCTTCAATAATCATGGCTTTAGAAACTCAGAAAAGGAG
GATAATGTGGATTAAAACTTAAGAGTTCTAACATCGCTCATAAATGTACAGATATGCAAA
TTCATAGCTCAATAAAGAAATCTGATACCTTACGACCAAAAAAAA

FIGURE 82

MSAAWIPALGLGVCLLLLPGPAGSEGAAPIAITCFTRGLDIRKEKADVLCPGGCCPLEEFSVY
GNIVYASVSSICGAAVHRGVISNSGGPVRVYSLPGRENYSSVDANGIQSMLSRWSASFTVT
KGKSSTQEATGQAVSTAHPPTGKRLKKTPEKKTGNKDCKADIAFLIDGSFNIGQRRFNLQKN
FVGKVALMLGIGTEGPHVGLVQASEHPKIEFYLNFTSAKDVLFAlKEVGFRRGNSNTGKAL
KHTAQKFFTVDAGVRKGIPKVVVVFIDGWPSDDIEEAGIVAREFGVNVFIVSVAKPIPEELG
MVQDVTFVDKAVCRNNGFFSYHMPNWFGTTKYVKPLVQKLCTHEQMMCSKTCYNSVNI AFLI
DGSSSVGDSNFRLMLEFVSNIAKTFEISDIGAKIAAVQFTYDQRTEFSFTDYSTKENVLAVI
RNIRYMSGGTATGDAISFTVRNVFGPIRESPNKNFLVIVTDGQSYDDVQGPAAAAHDAGITI
FSVGVAWAPLDDLKDMASKPKESHAFFTREFTGLEPIVSDVIRGICRDFLESQQ

Signal sequence:

amino acids 1-24

N-glycosylation site.

amino acids 100-104, 221-225

Casein kinase II phosphorylation site.

amino acids 102-106, 129-133, 224-228, 316-320, 377-381, 420-424,
425-429, 478-482, 528-532

N-myristoylation site.

amino acids 10-16, 23-29, 81-87, 135-141, 158-164, 205-211,
239-245, 240-246, 261-267, 403-409, 442-448, 443-449

Amidation site.

amino acids 145-149

FIGURE 83

CGCCGCGCTCCCGCACCCGCGGCCCGCCACCGCGCGCTCCCGCATCTGCACCCGAGCCC
GGCGGCCTCCCGGCGGGAGCGAGCAGATCCAGTCCGCGCCCGCAGCGCAACTCGGTCCAGTCG
GGCGCGCGCTGCGGGCGCAGAGCGGAGATGCGAGCGGCTTGGGGCCACCTCGTGTGCTGCCTGC
TGCTGGCGGCGCGGTCCCCACGGCCCCGCGCCCGCTCCGACGGCGACCTCGGTCCAGTCTC
AAGCCCCGGCCGGCTCTAGCTACCCGAGGAGGAGGCCACCTCAATGAGATGTTCCGCGA
GGTTGAGGAAGCTGATGGAGGACACGCGACACAAATTGCGCAGCGCGGTGGAAAGAGATGGAGG
CAGAAGAGCTGCTGCTAAAGCATCATCAGAAGTGAACCTGGCAAACTTACCTCCAGCTAT
CACAATGAGACCAACACAGACACGAAGTTGGAAATAATACCATCCATGTGCACCGAGAAAT
TCACAAGATAACCAACACAGACTGGACAAATGGTCTTTTCAGAGACAGTTATCACATCTG
TGGGAGACGAAGAAGGCAGAAGGAGCCACGAGTGCATCATCGACGAGGACTGTGGGCCACG
ATGTACTGCCAGTCTTGGCAGCTTCCAGTACACCTGCCAGCCATGCCGGGCCAGAGGATGCT
CTGCACCCGGGACAGTGAGTGTGTGGAGACCAGCTGTGTGTCTGGGGTCACTGCACCAAAA
TGGCCACCGGGGAGCAATGGGACCATCTGTGACAAACGAGAGGACTGCCAGCCGGGGCTG
TGCTGTGCTTCCAGAGAGGCGCTGTTCCTGTGTGTGCACACCCCTGCCGTGGAGGGCGA
GCTTGGCCATGACCCGCCAGCGGCTTCTGGACCTCATCACCTGGGAGCTAGAGCTGTATG
GAGCCTTGGACCGATGCCCTTGTGCCAGTGGCCTCCTTGCCAGCCCCACAGCCACAGCTCG
GTGTATGTGTGCAAGCCGACCTTCGTGGGGAGCCGTGACCAAGATGGGGAGATCCGTGCTGCC
CAGAGAGGTCCTCGATGAGTATGAAGTTGGCAGCTTCATGGAGGAGGTGCGCCAGGAGCTGG
AGGACCTGGAGAGGAGCCTGACTGAAGAGATGGCGTGGGGAGCTGCGGCTGCCCGCTG
GCACTGTCTGGAGGGGAAGAGATTAGATCTGGACCAGGCTGTGGGTAGATGTGCAATAGAA
ATAGCTAATTTATTTCCCGAGGTGTGTGCTTTAGGCGTGGGTGACAGGCTTCTTCCTACA
TCTTCTCCAGTAAGTTTCCCTCTGGCTTGACAGCATGAGGTGTTGTGCAATTTGTTTCAGC
TCCCCAGGCTGTTCTCCAGGCTTCACAGTCTGTGTCTGGGAGAGTCAGGCAGGGTTAAAC
TGCAAGGAGCAGTTTGGCACCCCTGTCCAGATTATTGGCTGCTTTGGCTCTACCAAGTTGGCAG
ACAGCCGTTTGTCTACATGGCTTTGATAATTGTTTGGGGGAGGAGATGGAAACAATGTGG
AGTCTCCCTCTGATTGGTTTTGGGGAATGTGGAGAAGAGTGCCCTCTTTTGCAAAACATCAA
CCTGGCAAAAATGCAACAAATGAATTTCCACGCAAGTCTTTCCATGGGCATAGGTAAGCTG
TGCTTCAGCTGTGTCAGATGAATGTTCTGTTCACCCCTGCATTACATGTGTTTATTCATCC
AGCAGTGTGCTCAGCTCCTACCTCTGTGCCAGGGCAGCATTTTCATATCCAAGATCAATTC
CCTCTCTCAGCACAGCCTGGGGAGGGGGTCATTGTTCTCCTCGTCCATCAGGGATCTCAGAG
GCTCAGAGACTGCAAGCTGCTTGGCCAAAGTCACACAGCTAGTGAAGACCAGAGCAGTTTCAT
CTGGTTGTGACTCTAAGCTCAGTGCTCTCTCCACTACCCACACCAGCCTTGGTGCCACCAA
AAGTGCTCCCCAAAAGGAAGGAGAATGGGATTTTCTTGAGGGCATGCACATCTGGAATTAAG
GTCAAACTAATTTCTACATCCCTCTAAAAGTAAACTACTGTTAGGAACAGCAGTGTCTCAC
AGTGTGGGGCAGCGCTCTCTTAATGAAGACAATGATATTGACACTGTCCCTCTTTGGCAGT
TGCAATTAGTAACCTTTGAAAGGTATATGACTGAGCGTAGCATACAGGTTAACTGCAGAAACA
GTACTTAGTAATTGTAGGGCGAGGATTATAAATGAAATTTGCAAAATCACTTAGCAGCAAC
TGAAGACAATTATCAACCACGTGGAGAAAAATCAACCGAGCAGGGCTGTGTGAAACATGGTT
GTAATATGCGACTGCGAACACTGAACCTCTACGCCACTCCACAATGATGTTTTCAGGTGTCA
TGGACTGTTGGCCACATGATTTCATCCAGAGTCTTAAAGTTTAAAGTTGCACATGATTGTA
TAAGCATGCTTCTTTGAGTTTATAATATGTATAAACATAAGTTGCATTAGAAATCAAGC
ATAAATCACTTCAACTGCAAAAAAAAAAAAAAAAAAAAAAAAAA

00002572-071001

FIGURE 84

MQRLGATLLCLLLAAAVPTAPAPAPTATSAFVKPGPALSYPQEEATLNEMFREVVEELMEDTQ
HKLRS AVEEMEAEEAAA KASSEVNLANLP SYHN ETNTDTKVGNN TIHVHREIHKITNNQTG
QMVFSETVITSVGDEEGRRSHECI IDEDCGPSMYCQFASFQYTCQPCR GQRM LCTR DSECCG
DQLCVWGHCTKMATRG SNGTICDNQRDCQPG LCCAFQ RGLLPVCTPLPVEGELCHDPASRL
LDLITWELEPDGALDRCP CASGLLCQPHSHSLVYVCKPTFVGS RDQDGEILLPREVPDEYEV
GSFMEEVRQELEDLERSL TEEMALGE PAAAAAALLGGEI

Signal sequence:

amino acids 1-19

N-glycosylation site.

amino acids 96-100, 106-110, 121-125, 204-208

Casein kinase II phosphorylation site.

amino acids 46-50, 67-71, 98-102, 135-139, 206-210, 312-316,
327-331

N-myristoylation site.

amino acids 202-208, 217-223

Amidation site.

amino acids 140-144

FIGURE 85

AAGGAGGCTGGGAGGAAAGGTTAAGAAAGGTTAGAGAACTACCTCACTCTCTGCGGCTCAGAAGGACTCTG
 AAGATAACAATAATTTCAGGCCATCCACTCTCCTTCCCTCCCAAACACACATGTGCATGTACACACACATACA
 CACACCTACACCTTCTCTCTCTTCACTGAAGACTCAGCTCACTCACTCTGTGAGCAGGTCATAGAAAGGACAC
 TAAAGCTTTAAGCAGCGCTGGCCATTACCTCTGCAGCTCTTTTGGCTTGTGTAGCTCAAAAATAGCTGGGAGGGG
 CCAGGCCAGGTGACTCACACTGTATCCAGCACTTTTGGGAGACCGGAGTCCAGATCACTGTAGGCTCAGGAG
 TTGCAGACAGGCTTGGCCAACTGGAGAAACCCCACTCTCTACTAAAAATACAAAAATTAGCCAGGAGTGGTGGC
 AGGTGCTGTATATCCAGCTACTCAGGTGGCTGAGCCAGGAGAATCGCTTGAATCCAGGAGCGGAGGATGCAGT
 CAGCTGAGTGCACCGTGCATCTCAGCCTGGGTGACAGAAAGAGACTCTGTCTCAAAACAAACAAACCGGGAGGA
 GGGGTAGATACCTCTCTCTCAACCTCTTAACTCTGCATCTCTTCTTCCAGGCTTGGCCCTGATGGGCGCTG
 GCAATGACTGAGCAGGCCACCCCGAGAGGACAGGAGAGAGAGGATATTTGAGGAGGGCCAGAAAGTGACCCCG
 GTGTAGAATGACTGCCCTGGGAGGGTGGTTCTTGGGCCCTGGCAGGGTGTCTGACCTTACCTGCAAAAACA
 AAGAGCAGGACTCCAGACTCTCTTGTGAATGGTCCCCTGCCCTGCAGCTCCACATGAGGCTTCTCGTGGCCCC
 ACTCTTCTGCTAGCTTGGGTGGCTGGTCCACTGCCACTGTGCCCGTGGTACCTTGGCATGTTCCCTGCCCCCCCTCA
 GTGTGCCCTGCCAGATCCGGCTCTGGTATACGCCCGCTCGTCTTACCAGGAGGCTACCATGTGGACTGCAATGA
 CTTATTCTGACGGCAGTCCCCCGGCACTCCCGCAGGCAACAGACCTGTCTCTCAGAGCAACAGCATTTGT
 CGGTGTGACAGGATGTAGCTGGGCTACCTGGCCAACTCTCAGAGACTGGACTGTCCCAAGACAGCTTTTCGGA
 TGCCTGAGTGTGATTTCCATGCCCTGGCCAGCTGCTGAGCTGCACCTAGAGGCTGAGCTGACCCGGCT
 GGAGGACCAAGCTTGTGAGGCTGGCCAGCTTCAAGAACTCTATCTCAACCAACACAGCTCTTACCGCATCGC
 CCCCAGGCGCTTTTCTGGCTCAGCAACTTGTCTGGCTGCACCTCAACTCTTCAAGGCTTCCAGGCGCATTTGACAG
 CGCTGGTTTGAATGCTGCCAACTTTGAGATACTCATGATTGGCGGCAACAGGTAGATGGCATCTCTGGACAT
 GAACTTCCGCGCCCTGGGCAACTGTGCTAGCTGGTGTCTAGCAGGCTGAACTCGGGGAGATCTCCGACATGCT
 CTTGGAGGGGCTGCAAGGCTTGGAGAGCTCTCTCTCTATGACAAACAGCTGGCCGGGTGGCCAGGCGGCACT
 GGAACAGGTGCCCGGCTCAAGTTCTTAGACTCAACAAGAACCCGCTCCAGCGGTGAGGCGGGGAGCTTTTGC
 CAACATGCTGCACCTTAAGAGAGCTGGGACTGAAACAACATGGAGGAGCTGGTCTCCATGCAGAACTTTCCTGTGT
 GAACTTCCCGAGCTGACCAAGCTGGACATCAACAATAACCCACGGCTGTCTTATCTTCCACCCCGGCTTTC
 CCACCTCCCGAGATGGAGAGCTCATGCTCAACAACAACGCTCTCAGTGCCTTGCACACAGCAGAGCGTGGAGTCA
 CTCTGCCAACCTCAGGAGGATGCTTCCACGCAACCCCACTCGCTGCTTGTGATCTGTCTCCCTGGGCGCATCGC
 CACGGGCAAGGCTGTCCCTTCTATCAGCCGCAATCCACCCTGTGTGCGAGCTCTCCGACCTTCCAGCGCTCTCC
 GGTGTGAGGCTGTCTTCTCGGAGAGATGACGAGCACTGTTTTCCTCTTCTTCCCAAGAGCTTCTCCCCCAAG
 CTCTCAGTGTGAGTGGAGAGACTGTGTCTGCTTGCCTGGCGGCTGGCCGAAACCCGAAACCCGAGATCTACTG
 GGTCACTCAGCTTGGCTTGCAGTACACTTGCCTTGCAGGACAGGAGGTACCGGTGTATCCCGGAGGGGACCTT
 GGAGCTGCGGAGGCTGACGACAGAGGCGCAGGCTATACACTGTGTGGCCAGAACCTGTGTGGGGCTGACAC
 TAAAGACGTTAGTGTGTGTGTGAGGCGCTCTCTCTCCAGCAGGACAGGACGAGGAGCAGGGGCTGGAGCTCG
 GTGTCAGGAGCAACCCCTATCACATCTGCTATCTTGGGTCAACCCACCCAGACAGATGTGTCCACCAACTCAC
 CTGGTGCAGTGGCTCTCTCTCCCGGGCAGGGGGCCACAGCTCTGGCCCGCTGCTCTCGGGGAACCCACAGTCA
 CAACTATACCCGCTCTTTCAGGCCAGGAGTACTGGGCTGCTTGCATGCTTGTGATGCCACACCTCA
 GTTGGCTGTGTATGGGCAAGGACAAAGAGGCACTTCTTGCCACAGAGCTTAGGGGATCGTCTGGGCTCAT
 TGCCATCTTGGCTCTCGCTGTCTTCTCTCTGGCAGCTGGGCTAGCGGCCCACTTGGCATGAGCCCAACCAAGAA
 GGGTGTGGTGGGAGCGGCTCTCTCTCAGCTTGGGCTTCTTGGGGCTGGAGTGGCCCTTCTGTCTGGGTTGT
 GTCTGCTCCCTCTCTGCCCTGGAATCCAGGAGGAAAGCTGCCAGATCTCTCAGAAAGGAGAGACTGTTGCC
 ACCATTGTCTCAAAATCTTGAAGCTCAGCTGTTCTCAGCAGTAGAGAAATCACTAGGACTACTTTTATACAAA
 AGAGAAGCAGTCTGGGCAAGTGCCTTCCAGGAAAGGACATGGACCCACGCTGTTGAGGCTGGCAGCTGGGCG
 CAAGCAGCAGTGGGCTTGTGGCCCTGGGGTGCTTCTGCAGGCTTGAAAGATTGCCCCCTTACCTCTAGAGGTCA
 CCTCTGTCTCATTTGAGAGAACTCAAGGAACAGGAGGACTTGGCTGATCTGTGCTTGCCTGCCCTCCCTCT
 TCTCTTCCAGAGCTCTTGGGCTTGGCTTGGCTGTCCCTACCTGTGTCCCGGGCTGCACCCCTTCTCTTCT
 TCTTCTGTGATCAGCTCTCAGTTGCTTGTCTTGTGCTCTTGGGCAAGGCTGAGGAGGCTCATCATCTCAC
 CTGGGGGGCTGCCCTCAATGTGGAGTGAACCCAGCCAGATCTGAAGGACATTTGGGAGAGGAGTGGCCAGGAA
 CGCTCATCTCAGCAGCTGGGCTGGCATTCGAAGCTGACTTTCTATAGGCAATTTGTACTTTTGTGGAGAA
 ATGTGTCACTCCCCAACCCGATTCACTCTTTCTCTGTTTGTAAAAATAAAAAATAATAATAACATATAA
 AAAA

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FIGURE 86

MRLLVAPLLLAUVAGATATVPVVPWHVPCPPQACQIRPWYTPRSSYREATTVDCNDLFLTA
VPPALPAGTQTLLQLQNSIVRVDQSELGYLANLTEDLSQNSFSDARDCDFHALPQLLSLHL
EENQLTRLEDHSFAGLASLQELYLNHNQLYRIAPRAFSGLSNLLRLHLNSNLLRAIDSRWFE
MLPNLEILMIGGNKVDAILDMNFRPLANLRSLVLAGMNLREISDYALEGLQSLSESLSFYDNQ
LARVPRRALEQVPGLKFLDLNKNPLQRVGPGDFANMLHLKELGLNNMEELVSDKFAVLVNL
ELTKLDITNNPRLSFIFHPRAFHHLPQMETMLNNNALSALHQQTVESLPLNQLQEVGLHGNPIR
CDCVIRWANATGTRVRFIEPQSTLCAEPPDLQRLPVREVPFREMTDHCPLISPRSFPSSLQ
VASGESMVLHCRALAEPEPEIYWVTPAGLRRLTPAHAGRRYRVYPEGTLELRRVTABEAGLYT
CVAQNLVGADTKTVSVVVGRALLQPGRDEGQGLELRVQETHPHYHILLSWVTPNTVSTNLTW
SSASSLRGQGATALARLPRGTHSYNITRLLQATEYWACLQVAFADAHTQLACVWARTKEATS
CHRALGDRPGLIAILALAVLLAAGLAHLGTGQPRKGVGGRRPLPPAWAFWGSAPSVRV
SAPLVLPWNPGRKLPSSSEGETLLPPLSQNS

Signal sequence:

amino acids 1-18

Transmembrane domain:

amino acids 629-648

N-glycosylation site.

amino acids 94-98, 381-385, 555-559, 583-587

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 485-489

Casein kinase II phosphorylation site.

amino acids 46-50, 51-55, 96-100, 104-108, 130-134, 142-146,
243-247, 313-317, 488-492, 700-704

Tyrosine kinase phosphorylation site.

amino acids 532-540

N-myristoylation site.

amino acids 15-21, 493-499, 566-572

Amidation site.

amino acids 470-474, 660-664, 692-696

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100	101	102	103	104	105	106	107	108	109	110	111	112	113	114	115	116	117	118	119	120	121	122	123	124	125	126	127	128	129	130	131	132	133	134	135	136	137	138	139	140	141	142	143	144	145	146	147	148	149	150	151	152	153	154	155	156	157	158	159	160	161	162	163	164	165	166	167	168	169	170	171	172	173	174	175	176	177	178	179	180	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195	196	197	198	199	200	201	202	203	204	205	206	207	208	209	210	211	212	213	214	215	216	217	218	219	220	221	222	223	224	225	226	227	228	229	230	231	232	233	234	235	236	237	238	239	240	241	242	243	244	245	246	247	248	249	250	251	252	253	254	255	256	257	258	259	260	261	262	263	264	265	266	267	268	269	270	271	272	273	274	275	276	277	278	279	280	281	282	283	284	285	286	287	288	289	290	291	292	293	294	295	296	297	298	299	300	301	302	303	304	305	306	307	308	309	310	311	312	313	314	315	316	317	318	319	320	321	322	323	324	325	326	327	328	329	330	331	332	333	334	335	336	337	338	339	340	341	342	343	344	345	346	347	348	349	350	351	352	353	354	355	356	357	358	359	360	361	362	363	364	365	366	367	368	369	370	371	372	373	374	375	376	377	378	379	380	381	382	383	384	385	386	387	388	389	390	391	392	393	394	395	396	397	398	399	400	401	402	403	404	405	406	407	408	409	410	411	412	413	414	415	416	417	418	419	420	421	422	423	424	425	426	427	428	429	430	431	432	433	434	435	436	437	438	439	440	441	442	443	444	445	446	447	448	449	450	451	452	453	454	455	456	457	458	459	460	461	462	463	464	465	466	467	468	469	470	471	472	473	474	475	476	477	478	479	480	481	482	483	484	485	486	487	488	489	490	491	492	493	494	495	496	497	498	499	500	501	502	503	504	505	506	507	508	509	510	511	512	513	514	515	516	517	518	519	520	521	522	523	52
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CGAAGCAGCGGCGCGCTGTGTGAGAAGGTGAGAAGATTCCGGACCCATGTGGAGGAGGGGGACATTGTGTACCGCCT
 CATATCGCGGACGACCATCATCAAGGTGTCAAGTGTTCATCTCTCATCTGCTACACCGCTCTACTACGTGTGCACAA
 CATCAAGTTCGACCTGGACTGCACCGTGGACATTGAGAGCTGACGGGGTACCGCACCTACCGCTGTGCCACCC
 CCGTGGCCACATCTCTCAAGTCTGTGGCTGTCTTCATACATGACCTTAGTCATCTTACCGCCTCATTCTGCATGTGA
 CACACTGTGTGTGGATGTACTCGCGCTCCCTCAAGATGACTCGTTTGAGTCGATCCGTGAGGAGAGAGCGCTACGAC
 CGACATCCCGCGAGCTCGAAGAACGATCTCGCCTCTCATGTCTGCACTCATTTGACCAATACGACCCGCTCTACTCTCAA
 CGCGTTCGCGCTCTCTCTGTGCGAGGTGAGTGAGAACAAAGCTCGGGACGCTGAACTCAACAAAGCATGTGAAGCT
 CGACAAAGCTCCGGGACGGGCTCA CCAAGAAACGCGGAGAACAGCTTGAGAGCTGCACCTGTCTCATGTCTCAGTGGCC
 CCTCGACACTGTGTTTGAACCTGTGTGGAGCTGGAGGTCCTCAAGCTGTAGCTGATCCCGAGCTGACCATCCCGCC
 CAGCATGTTGCCAGCTCA CGGGCTCAAGGAGCTGTGGCTTTACACACAGCGGCCAAGATTGAAGCGCTGTGCTGT
 GCGCTTCTCGCGAGAACTCTGGGGCGCTGCACATCAAGTTACACGCACATCAAGAGATCTCCGCTGCTGATCTTA
 TAGCTCGAAGACATGTGAGGAGCTGCACCTGACGCGGCAACTTGAGCGCGGAGAACAAACCGCTACATCTGTCATCGA
 CGGGCTCGGGAGCTCAAAACGCTCAAGTGTGCTGGCTCTCAAGACAGCTTAAGAACCTGCCAACAGGTGTGTCA
 AGATGTGGGCTGTGCACCTGACAGAGCTGTCTTCATCAACAATGAGGGCAACAGCTCATCTGCTCTCAACGGCTCAA
 GAAGATGGGCAACCTGATCGAGCTGAGCTGATCTCGCTGCAACTGTGAGCGACTCCCCCACTCATCTTCAGCTCT
 CCAACAACTCGAGGAGATTAAGCTCTCAAGGACAACCAACTCAAGACCATGCGAGAGATCATCAGCTCTCAGACGCTCAA
 GCACCGCTCAGCTGCTTGTGCTGTGGTACCAACTGCTGCATACCTCCCTACAGATCGGCAACTGCCAACCTCCAA
 CTGAGGCGCCTCTACTCTGACACCGCAACAGATGAGAAGATCCCCACCGACTCTCTACTGCGCCAGCTGCG
 CTACTGGACTCAGCACAACAACTGACCTTCTCTCCGCAACTCGGCTCTCTGCAAGCTCGAGCTGTGTGTGGAGAA
 CCAACGGCTCAGACAGCTGCTGCTGTGAGACTGGGCGAGTCCCACTGACAACTGACGAGATCGAGTGTGCGGGG
 GCACTGTTCAACATCGATCCGCAACCGGAGTGAAGGCGCGCTGTGAGGGCTGACAAAGAGACAGCGCTGAGCGAG
 ACCTCTCCGACAGCCAGGACAGCCCTTCGCGCTGGGCGAGGAGCTGTGGAGGCTGACAAAGCGAGCGCTGAGCGAG
 GGACAGTATCTGTGGGCTGCGCTTCTTCTCTGAGACTACGCTCCCGAGGGGCAAGTGTCTGTGAGAGAG
 AGCAAGTCTCAAGAGCGCATTTTGGATTAATCAGGCTCTCTCTCGAGGACAGCTCTGCGCCAGGCGGAGTGAG
 CTGCGACAGAGGCTCTGGGACCTCACTTTAGTTCTTGTTATTTATTTCTTCATCTCCCACTCTCTTCACTC
 AGATACTGTATATACATCTCCAGAAAGTTTCAGCCACAGCTGGAAGGTGTACAGGAAAGTGTGGGCTGCTTCTCCCT
 TTGTCTTATTTAGOGATCGCGCGGGCATTTAAACCCACTGGACTCTGACAGAGTGTGCGGCGGCAACAG
 CCAATGGAGCGCTCAGCAGGATCGCGGCTGGGCTCTCGGCTCGGCTCCAGCGAGAGAGCGAGCTCCAGCTGGT
 AAGCGAGCGCTGAGACTGTGCTCTTCAGTTTTGTGCAATTTTAGTTTTGTTTTTTTTTTAAATAAA
 AAAACAATTTTTTTTTAAAAAAAGTTTGAAATTGGATGTTTGGGTATTAATAAAGAAAAAAATCTAAAAAA
 AAAAGACATAACCGCCAGTGAAGTTGAGCTTCAGGCGAGGGGGGAGGATTTCTTGAGCAAGCAGCAGAGCT
 TGAATCTGTGTCTCTTCTCGGCGCAGGGTGCAGGGTGTCTCGGATCTGGTGTGACCTTGTGTCAGAGGT
 CTATTGTGTTCTGGGAGGAGGTTTTTTTGTGTTTGTGTTTTTTGTTTTTTGTTGTTCTGTTTCTCTCTCTC
 ATGTGCTTGGCAGGACTCAATTCTGTGCTGTCTGCCAGAGGGAATGTTCTGGAGCTGCCAAGGAGGAGGAG
 ACTCGGTTGTGACATACTCCCGAGTAAACGCTGCTGCATTCGCACTCCCTCTCTGCTGCTGCTGCTCTTCA
 CGCACTGCTGTGAAGGACCAAGAGGAGCACTCTGCCAGACTTGTGTTCCCACTCTCGCGGACAGGTTGTGT
 CCAGTGCACGCTGTGCTCTCGCTGCTCTACATCGACTGTGCGCACTGGTGTCTATGAAGACAGGACTTTA
 GAGCTGTGTCGGGAATGGGAGGCTCGCCCTGGAGGCGAGGCGTGTGTTCAAGCCGGTTCGGCTCTCCCTGGGC
 CTGAGTGTGACACAGCCAGCTGCGCACCTGGTGGTGAAGAACCACTGCTTTAGATCACTCCGCTCCCACTCT
 AGAAGGCTCCCGCTTTAGATCAATCTCTGCGACTCAAGGACAGCTTTAGAGATCTCTGTCTTAATGATTATGT
 CCATCGCTCTGTCTGCTCAATTGTGTTTCTGTGCTGTCTCATTGATATACTCGAATAATATGACACTAG
 CTTCTGACAACTATGAAGCAAAAAATCCGTTTACGTGGGTCTGAACTTGTAGACTCGGTACAGTATCAAATAAA
 ACTTATACAGGAAAAAAAAAAA

FIGURE 88

MRQTIKVIKFIILICYTVYYVHNKFDVDCITVDIESLTGYRTYRCAHPLATLFKILASFYI
SLVIFYGLICMYTLWWMLRRSLKKYSFESIREESSYSDIPDVKNDFAFMLHLIDQYDPLYSK
RFAVFLSEVSENKLRQLNLNNEWTLDKLRQRLTKNAQDKLELHLFMLSIGIPDTVFDLVELEV
LKLELIPDVTIPPSIAQLTGLKELWLYHTAAKIEAPALAFLENLRAHLEHIKPTDIKEIPLWI
YSLKTLEELHLTGNLSAENNRYIVIDGLRELKRLKVLRLKSNLSKLPQVVTDVGVHLQKLSI
NNEGTKLIVLNSLKKMANLLELELIRCDLERIPHSIFSLHNLQIDLDKNNLKTIEEIIISFQ
HLHRLTCLKLWYNHIAIPIQIGNLTNLERLYLNRNKIEKIPTQLFYCRKRLYLDLSHNNLT
FLPADIGLLQNLQNLAITANRIETLPPPELFQCRKLRLHLGNVQLSLSRVRGELTNLTQIE
LRGNRLECLPVELGECPLLKRSGLVVEEDLFNTLPPPEVKERLWRADKEQA

Transmembrane domain:

amino acids 51-75 (type II)

N-glycosylation site.

amino acids 262-266, 290-294, 328-332, 396-400, 432-436, 491-495

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 85-89

Casein kinase II phosphorylation site.

amino acids 91-95, 97-101, 177-181, 253-257, 330-334, 364-368,
398-402, 493-497

N-myristoylation site.

amino acids 173-179, 261-267, 395-401, 441-447

FIGURE 89

GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTCAATGGAGCTGGCACTGCGGCGCTCTCCCGT
CCCCGGTGGTTGCTGCTGCTGCCGTGCTGCTGGGCCTGAACGCAGGAGCTGTCAATTGACT
GGCCCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCCATACATG
TTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCCTGGTCAT
GTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTGGAAACTTTGAGGAAATGGGC
CCCTTGACAGTGATCTCAAACCACGGAAAACCACTGGCTCCAGGCTGCCAGTCTCCTATTT
GTGGATAATCCCGTGGGCACTGGGTTCA GTTATGTGAATGGTAGTGGTGCTATGCCAAGGA
CCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTCTTCAGTTGCCACAAAG
AATTCAGACAGTTCATTTCTACATTTTCTCAGAGTCCATGGAGGAAAAATGGCAGCTGGC
ATTGGTCTAGAGCTTTATAAGGCCATTACAGCAGGGACCATCAAGTGCAACTTTGCGGGGGT
TGCCTTGGGTGATTCTCGATCTCCCTGTGTGATTCCGTGCTCTCCTGGGGACCTTACCTGT
ACAGCATGTCTTTCTCGAAGACAAAGTCTGCGCAGAGGTGTCTAAGGTTGCAGAGCAAGTA
CTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCCACAGAGCTGGGGGAAAGCAGAAAT
GATCATTGAACAGAACACAGATGGGGTGAACCTCTATAACATCTTAAGTAAAAGCATCCCA
CGCTACAATGGAGTCGAGTCTAGAATTCACACAGAGCCACCTAGTTTGTCTTTGTCAGCGC
CACGTGAGACACCTACAACGAGATGCCTTAAGCCAGCTCATGAATGGCCCCATCAGAAAGAA
GCTCAAAATTATTCCTGAGGATCAATCCTGGGGAGGCCAGGCTACCAACGCTTTTGTGAACA
TGGAGGAGGACTTCATGAAGCCAGTCATTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATC
AACGTGACGGTGTATAATGGACAGCTGGATCTCATCGTAGATACCATGGGTGAGGAGCCTG
GGTGCAGGAACTGAAGTGCCAGAACTGCCTAAATTCAGTCAGCTGAAGTGAAGGCCCTGT
ACAGTGACCTAAATCTTTGGAACATCTGCTTTTGTCAAGTCTTACAAGAACCTTGCTTTC
TACTGGATTCTGAAAGCTGGTCAATATGGTTCCTTCTGACCAAGGGGACATGGCTCTGAAGAT
GATGAGACTGGTGACTCAGCAAGAATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCT
TGGGGCACAGAGCTGAGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCT
AACTGGGGCTGTGATCAAGAAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCT
GGAGGCAATTGGAAATTATTTCTGCTTCTTAAAAAACCTAAGATTTTAAAAAAATTGAT
TGTTTTGTATCAAAATAAGGATGATAATAGATATTAA

FIGURE 90

MELALRRSPVPRWLLLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATNSC
KNFSELPLVMWLQGGPGGSSSTGFGNFEEIGPLDSDLKPRKTTWLQAASLLFVDNPNVGTGFSY
VNGSGAYAKDLAMVASDMMVLKTFFSCHKEFQTVPFYIFSESYGKKMAAGIGLELYKAIQR
GTIKCNFAGVALGDSWISPVDSVLSWGPYLYSMSLLEDKGLAEVSKVAEQVLNAVNGGLYRE
ATELWGKAEMII EQNTDGVNFYNILTKSTPTSTMESSLEFTQSHLVCLCQRHVRHLQRDAL
QLMNGPIRKKLKIIPEDQSWGQATNVFVNMEEDFMKPVISIVDELLEAGINVTIVYNGQLDL
IVDTMGQEAWVRKLKWPPELPKFSQLKWKALYSDEPKSLETSAPVKSYNLAFYWILKAGHMVP
SDQGDMLKMMRLVTQQE

Signal sequence:

amino acids 1-25

N-glycosylation site.

amino acids 64-68, 126-130, 362-366

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 101-105

Casein kinase II phosphorylation site.

amino acids 204-208, 220-224, 280-284, 284-288, 351-355, 449-453

N-myristoylation site.

amino acids 22-28, 76-82, 79-85, 80-86, 119-125, 169-175,
187-193, 195-201, 331-337, 332-338, 360-366

GGCCGCGGGAGAGGAGGCCATATGGGCGCGCGCGGGGCGCTGCTGCTGGCGCTGCTGCTGGCTCT
GGGCTGGACTCAGGAAGCCGGAGTCGCAGGAGGCGGCGCCGTATCAGGACCATGCGGCCGA
CGGGTCATCACGTCGCGCATCGTGGGTGGAGAGGACGCCAACTCGGGCGTTGGCCGTGGCA
GGGGAGCCTGCGCCTGTGGGATTCACAGTATGCGGAGTGAGCCTGCTCAGCCACCGCTGGG
CACTCAGCGCGGCGCACTGCTTTGAAACCTATAGTGACCTTAGTGATCCTCCGGGTGGATG
GTCAGTTTGGCCAGCTGACTTCCATGCCATCCTTCTGGAGCCTGCAGGCCTACTACACCCG
TTACTTCGTATCGAATATCTATCTGAGCCCTCGCTACCTGGGGAATTACCCCTATGACATTG
CCTTGGTGAAGCTGTCTGCACCTGTACCTTACATAAACACATCCAGCCCATCTGTCTCCAG
GCCTCCACATTTGAGTTTGAGAACCGGACAGACTGCTGGGTGACTGGCTGGGGGTACATCAA
AGAGGATGAGGCACTGCCATCTCCCCACACCTCCAGGAAGTTCAGGTGCGCCATCATAAACA
ACTCTATGTGCAACCACCTCTTCCTCAAGTACAGTTTCCGCAAGGACATCTTTGGAGACATG
GTTTGTGCTGGCAAACGCCAAGGCGGGAAGGATGCCTGCTTCGGTGACTCAGGTGGACCCCT
GGCCTGTAAACAAGAAATGGACTGTGGTATCAGATTGGAGTCGTGAGCTGGGGAGTGGGCTGTG
CTGGGCCCAATCGGCCCGGTGCTACACCAATATCAGCCACCACTTTGAGTGGATCCAGAAG
CTGATGGCCAGGAGTGGCATCTCCAGCCGACGCCCTCTGGACCTACTCTTTTTCCCTCT
TCTCTGGGCTCTFCCCATCTCTGGGCCGGCTGTGAGCCTACCTGACCCATGCAGCCTGGGG
CACTGCCAAGTCAGGCCTGGTCTCTTCTGTCTTGTGTTGGTAATAAACACATTCCAGTTGA
TGCTTGCAGGCATCTCTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 92

MGARGALLALLARAGLRKPESQEAAPLSGPGRRVITSRIVGGEDAELGRWPWQGSRLRW
DSHVCVGSLLSHRWALTAACHFETYSDLSDFSGWMVQFGQLTSMPSFWSLQAYYTRYFVSNI
YLSPRYLGNSPYDIALVKLSAPVTTYTKHIQPICLQASTFEFENRTDCWVTGWGYIKEDEALP
SPHTLQEVQVAIINNSMCNHLFLKYSFRKDI FGDMVCAGNAQGGKDACFGDSGGPLACNKNG
LWYQIGVVSWSGVGCGRPNRPGVYTNISHHFEWIKLMAQSGMSQPDPSWPLLFFPLLWALPL
LGPV

Signal sequence:

amino acids 1-18

N-glycosylation site.

amino acids 167-171, 200-204, 273-277

Casein kinase II phosphorylation site.

amino acids 86-90, 134-138, 161-165, 190-194, 291-295

N-myristoylation site.

amino acids 2-8, 44-50, 101-107, 225-231, 229-235, 239-245,
259-265, 269-275

Amidation site.

amino acids 33-37

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 252-263,

Serine proteases, trypsin family, histidine active site.

amino acids 78-84

FIGURE 93

CCCACGCGTCCGCGGACGCGTGGGAAGGGCAGAAATCGGACTCCAAGCCTGCCTCCTAGGGCT
CTTTGCCCTCATCTCTCTGCGCAAATGCAGTTACAGCCCCGAGCCCCGACCGGAGGAGCGC
TGCCCCCAGGCTGGGTGTCCCTGGGCCGTGCGGACCCTGAGGAAGAGCTGAGTCTCACCTTT
GCCCTGAGACAGCAGAAATGTGGAAGAGCTCTCGGAGCTGGTGCAGGCTGTGTGCGGATCCAG
CTCTCCTCAATACGGAATAACCTGACCTTAGAGAATGTGGCTGATCTGGTGAGGCCATCCC
CACTGACCCTCCACACGGGTGCAAAAATGGCTCTTGGCAGCCGGAGCCAGAAAGTGCCATTCT
GTGATCACACAGGACTTTCTGACTTGCTGGCTGAGCATCCGACAAAGCAGAGCTGCTGCTCCC
TGGGCTGAGTTTCACTACTATGTGGGAGGACCTACGGAACCACATGTTGTAAGGTCCCCAC
ATCCCTACCACTTCCACAGGCCCTTGCCCCCAATGTGGACTTTGTGGGGGGACTGCACCGT
TTTCCCCCAACATCATCCTGAGGCAACGCTCTGAGCCGAGGTGACAGGGACTGTAGGCCT
GCATCTGGGGGTAAACCCCTCTGTGATCCGTAAGCGATAACAACCTTGACCTCACAAGACGTGG
GCTCTGGCACCAGCAATAACAGCCAAGCCTGTGCCAGTTCTTGAGGCAGTATTTCCATGAC
TCAGACCTGGCTCAGTTTCATGCGCCTCTTCGGTGCAACTTTGCACATCAGGCATCAGTAGC
CCGTGTGGTTGGACAACAGGGCCGGGGCCGGGCGGAGTTGAGGCAGTCTAGATGTGCAGT
ACCTGATGAGTGCTGGTGCCAAACATCTCCACCTGGGTCTACAGTAGCCCTGGCCGGCATGAG
GGACAGGAGCCCTTCTCGAGTGGCTCATGCTGCTCAGTAATGAGTCAGCCCTGCCACATGT
GCATACTGTGAGCTATGGAGATGATGAGGACTCCCTCAGCAGCGCCTACATCAGCGGGTCA
ACACTGAGCTCATGAAGGCTGCCGCTCGGGGTCTCACCTTGCTCTTCGCCCTCAGGTGACAGT
GGGCGCGGTGTGTGGTCTGTCTCTGGAAGACACAGTTCCGCCCTACCTTTCCCTGCCTCAG
CCCTATGTCAACCACAGTGGGAGGCACATCCTTCCAGGAACCTTTTCCTCATCACAATGAAA
TTGTTGACTATATCAGTGGTGGTGGCTTCAGCAATGTGTTCACCGGCCCTCATACAGGAG
GAAGCTGTAACGAAGTTTCTGAGCTCTAGCCCCACCTGCCACCATCAGTTACTTCAATGC
CAGTGGCCGTGCCTACCCAGATGTGGCTGCACTTTCTGATGGCTACTGGGTGGTCAGCAACA
GAGTGCCCATTCCTGCGGTGTCGGAACCTCGGCCCTCTACTCCAGTGTTTGGGGGATCCTA
TCCTTGATCAATGAGCACAGGATCCTTAGTGGCCGCCCCCTCTGGCTTTCTCAACCCAAG
GCTCTACCAGCAGCATGGGGCAGGTCTCTTTGATGTAACCCGTGGCTGCCATGAGTCTCTGTG
TGGATGAAGAGGTAGAGGGCCAGGGTTTCTGCTCTGGTCTGGCTGGGATCCTGTAAACAGC
TGGGGAACCAACCTTCCAGCTTTGCTGAAGACTCTACTCAACCCCTGACCCTTTCTCATC
AGGAGAGATGGCTTGTCCCTGCCCTGAAGCTGGCAGTTTCAGTCCCTTATTCTGCCCTGTG
GAAGCCCTGCTGAACCCCTCAACTATTGACTGCTGCAGACAGCTTATCTCCCTAACCCCTGAAA
TGCTGTGAGCTTGACTTGACTCCCAACCTTACCATGCTCCATCATACTCAGGTCTCCCTACT
CTGCTTAGATTCTCTCAATAAGATGCTGTAAGTACTGATTTTGAATGCCCTCTCCCTCCG
ATCTCATCTTTCTCTTTTCAATCAGGCTTTTCCAAAGGGTTGTATACAGACTCTGTGCACTA
TTTCACTTGATATTCATTTCCCAATTCACTGCAAGGAGACCTCTACTGTCAACCGTTTACTCT
TTCTACCTTGACATCCAGAAACAAATGGCCTCCAGTGATATCTTCACTTTGCTTTTATG
GCCTTTCCATCATAGTTGCCACTCCCTCTCTTACTTACTGCTTCCAGGTCTTAACTTCTCTG
ACTACTCTTGCTTCTCTCTCATCAATTTCTGCTTCTTCATGGAATGCTGACCTTCATTGC
TCCATTTGTAGATTTTCTCTTTCTCAGTTTACTCATTTGCCCTGGAACAAATCAACTGACA
TCTACAAACATTACCATCTCACTAATAAGACTTTCTATCCAATAATGATTGATACCTCAA
TGTA

FIGURE 94

MGLQACLLGLFALILSGKCSYSPEPDQRRTLPPGWVSLGRADPEEELSLTFALRQQNVERLS
ELVQAVSDPSSPQYGYKYLLENVADLVRPSPFLTLHTVQKWLAAQAQKCHSVITQDFLTCLWL
SIRQAELLLPGAEBFHHYVGGFTETHVVRSPHPYQLPQALAPHVDFVGGGLHRFPPTSSLRQRP
EPQVTGTVGLHLGVTSPVIRKRYNLTSQDVGSGTSNNSQACAQFLEQYFHDSDLAQFMRLLFG
GNFAHQASVARVVGQGRGRAGIEASLDVQYLSAGANISTWVYSSPGRHEGQEPFLQWLML
LSNESALPHVHTVSYGDDEDSLSSAYIQRVNTELMKAAARGLTLLFASGDSGAGCWSVSGRH
QFRPTFPASSPYVTTVGGTSTFQEPFLITNEIVDYISGGGFSNVFPRPSYQEEAVTKFLSSSP
HLPPSSYFNASGRAYPDVAALSDGYWVVSNRVPIPWVSGTSASTPVFGGILSLINEHRILSG
RPPLGLFLNPRLYQQHGAGLFDVTRGCHESCLDEEVEGQGFCSGPGWDVPTGWGTPTSQLC

Signal sequence:

amino acids 1-16

N-glycosylation site.

amino acids 210-214, 222-226, 286-290, 313-317, 443-447

Glycosaminoglycan attachment site.

amino acids 361-365, 408-412, 538-542

Casein kinase II phosphorylation site.

amino acids 212-216, 324-328, 392-396, 420-424, 525-529

N-myristoylation site.

amino acids 2-8, 107-113, 195-201, 199-205, 217-223, 219-225,
248-254, 270-276, 284-290, 409-415, 410-416, 473-479, 482-488,
521-527, 533-539, 549-555

FIGURE 95

GCCGCGCGCTCTCTCCCGCGCCACACCTGTCTGAGCGGCGCAGCGAGCCGCGGCCCGGGC
GGGTGCTCGGCGCGGAACAGTGCTCGGCATGGCAGGGATTCCAGGGCTCTCTTCTCTCTC
TTCTTTCTGCTCTGTGCTGTGTTGGCAAGTGAGCCCTTACAGTGCCCCCTGGAAACCACTTG
GCCTGCATACCGCCTCCCTGTGCTCTTGCCCCAGTCTACCTCAATTTAGCCAAGCCAGACT
TTGGAGCCGAAGCCAAATTAGAAGTATCTTCTTCATGTGGACCCAGTGTCTATAAGGGAAGT
CCACTGCCCACTTACGAAGAGGCCAAGCAATATCTGTCTTATGAAACGCTCTATGCCAATGG
CAGCCGCACAGAGACGCAAGTGGGCATCTACATCCTCAGCAGTAGTGGAGATGGGGCCCAAC
ACCGAGACTCAGGGTCTTCAGGAAAGTCTCGAAGGAAGCGGCAGATTATGGCTATGACAGC
AGGTTCAGCATTTTTGGGAAGGACTTCTGTCTCACTACCCCTTCTCAACATCAGTGAAGTT
ATCCACGGGCTGCACCGGCACCCCTGGTGGCAGAGAAGCATGTCTCAGAGCTGCCCACTGCA
TACACGATGAAAAACCTATGTGAAAGGAACCCAGAAGCTTCGAGTGGGCTTCTCTAAAGCCC
AAGTTTAAAGATGGTGGTCGAGGGGCCAACGACTCCACTTCAGCCATGCCGAGCAGATGAA
ATTTCACTGGATCCGGGTGAAACGCACCCATGTGCCCAAGGGTTGGATCAAGGGCAATGCCA
ATGACATCGGCATGGATTATGATTATGCCCTCCTGGAACCTCAAAAAGCCCCACAAGAGAAAA
TTTATGAAGATTGGGGTGAGCCCTCCTGCTAAGCAGCTGCCAGGGGGCAGAATTCACCTTCTC
TGGTTATGACAAATGACCGACCAGGCAATTTGGTGTATCGCTTCTGTGACGTCAAAGACGAGA
CCTATGACTTGTCTTACCAGCAATGCGATGCCCAGCCAGGGGCCAGCGGCTTGGGGTCTAT
GTGAGGATGTGGAAGAGACAGCAGCAGAAGTGGGAGCGAAAAATTATGGCATTTTTTCAGG
GCACCACTGGGTGGACATGAATGGTTCCCCACAGGATTTCAACGTGGCTGTGAGAATCACTC
CTCTCAAATATGCCAGATTGTCTATTGGATTAAAGGAACTACCTGGATTGTAGGGAGGGG
TGACACAGTGTTCCCTCCTGGCAGCAATTAAGGGTCTTCATGTTCTATTTTAGGAGAGGCC
AAATTGTTTTTTGTCAATTGGCGTGACACAGTGTGTGTGTGTGTGTGTGTGTGTGAAGGTGT
CTTATAATCTTTTACCTATTTCTTACAATTGCAAGATGACTGGCTTTACTATTTGAAAACCTG
GTTTGTGTATCATATCATATATCATTTAAGCAGTTTGAAGGCATACTTTTGATAGAAAATAA
AAAAAATACTGATTTTGGGGCAATGAGGAATATTTGACAATTAAGTTAATCTTCACGTTTTTG
CAAACCTTGATTTTATTTCACTGTGAATGTTTCAAGATTTATATTAATATTTGGCATA
CAAGAGATATGAAAAAAAAAAAAAAAAA

FIGURE 96

MAGIPGLLFLFLFLLCAVGQVSPYSAPWKPTWPAYRLPVVLQSTLNLAKPDPFGAEAKLEVS
SSCGPQCHKGTPLPTYBEAKQYLSYETLYANGSRTETQVGIIYLSSSGDGAQHRDSGSSGKS
RRKRQIYGYSRFSIFGKDFLLNYPFSTSVKLSTGCTGTLVAEKHVLTAAHCIHDGKTYVKG
TQKLRVGFLLKPKFKDGGRGANDSTSAMPEQMKFQWIRVKRTHVPKGWIKGNANDIGMDYDYA
LLELKKPKRKRKFMKIGVSPPAKQLPGGRIHFGYDNDRPGNLVYRFCDVKDETYDLLYQQCD
AQPGASGSGVYVRMWKRQQQKWERKIIIGIFSGHQWVDMNGSPQDFNVAVRITPLKYAQICYW
IKGNYLDCREG

Signal sequence:

amino acids 1-19

N-glycosylation site.

amino acids 93-97, 207-211

Glycosaminoglycan attachment site.

amino acids 109-113, 316-320

Casein kinase II phosphorylation site.

amino acids 77-81, 95-99, 108-112, 280-284, 351-355

N-myristoylation site.

amino acids 159-165, 162-168, 202-208, 205-211, 314-320, 338-344

Serine proteases, trypsin family, histidine active site.

amino acids 171-177

FIGURE 97

GCATCGCCCTGGGTCTCTCGAGCCTGCTGCCTGCTCCCCGCCCCACCAGCCATGTGGTGT
CTGGAGCGCCCCAGCCCTGGGTGGGGGCTGTCTCGGCACCTTCACCTCCCTGCTGCTGCTG
GCGTCGACAGCCATCTCTCAATGCGGCCAGGATACCTGTTCCCCAGCCTGTGGGAAGCCCCA
GCAGCTGAACCGGGTTGTGGGCGGCGAGGACAGCACTGACAGCGAGTGGCCCTGGATCGTGA
GCATCCAGAAGAATGGGACCCACCACTGCGCAGGTTCTCTGCTCACCAGCCGCTGGGTGATC
ACTGCTGCCACTGTTTCAAGGACAACCTGAACAAACCATACCTGTTCTCTGTGCTGCTGGG
GGCCTGGCAGCTGGGGAACCCCTGGCTCTCGGTCCCAGAAGGTGGGTGTTGCCTGGGTGGAGC
CCCACCCCTGTGATTCTCTGGAAGGAAGTGCCTGTGCAGACATTGCCTGGTGCCTCTCGAG
CGCTCCATACAGTTCTCAGAGCGGGTCTGCCCATCTGCCTACCTGATGCCTCTATCCACCT
CCCTCAAACACCCACTGCTGGATCTCAGGCTGGGGGAGCATCCAAGATGGAGTTCCTTGC
CCCACCTCAGACCCTGCAGAAGCTGAAGGTTCTATCATCGACTCGGAAGTCTGCAGCCAT
CTGTACTGGCGGGGAGCAGGACAGGGACCCATCACTGAGGACATGCTGTGTGCCGGCTACTT
GGAGGGGAGCGGGATGCTTGTCTGGGCGACTCCGGGGGCCCCCTCATGTGCCAGGTGGACG
GCGCCTGGCTGCTGGCCGGCATCATCAGCTGGGGCGAGGGCTGTGCCGAGCGCAACAGGCC
GGGGTCTACATCAGCCTCTCTGCGCACCGCTCCTGGGTGGAGAAGATCGTGCAAGGGGTGCA
GCTCCGCGGGCGCGCTCAGGGGGGTGGGGCCCTCAGGGCACCGAGCCAGGGCTCTGGGGCCG
CCGCGCGCTCCTAGGGCGCAGCGGGACGCGGGGCTCGGATCTGAAAGGCGGCCAGATCCACA
TCTGGATCTGGATCTGCGGCGGCCTCGGGCGGTTTCCCCCGCGTAAATAGGCTCATCTACC
TCTACCTCTGGGGGCCCCGACGGCTGCTGCGAAAGGAAACCCCTCCCCGACCGCCCGAC
GGCCTCAGGCCCCCTCCAAGGCATCAGGCCCGCCCAACGGCTCATGTCCCCGCCCCAC
GACTTCCGGCCCCCCCCGGGCCCCAGCGCTTTTGTGTATATAAATGTTAATGATTTTAT
AGGTATTGTAAACCTGCCACATATCTTATTTATCTCTCAATTTCAATAAATTATTTATT
CTCCAAAAA

FIGURE 98

```
></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA43318
><subunit 1 of 1, 317 aa, 1 stop
><MW: 33732, pI: 7.90, NX(S/T): 1
MVVSGAPPALGGGCLGTFSTLLLLLASTAILNAARIPVPPACGKPPQLNRVVGGEDSTDSEWP
WIVSIQKNGTHHCAGSLLTSRWVITAAHCFKDNLNKPYLFVLLGAWQLGNPGSRSQKVGVA
WVEFHPVYSWKEGACADIALVRLERSIQFSERVLPICLPDASIHLPPNTHCWISGWGSIQDG
VPLPHPQTLQKLKVPIDSEVCSHLYWRGAGQGPTEDMLCAGYLEGERDACLGDSSGGPLMC
QVDGAWLLAGIISWGECAERNRPGVYISLSAHRSWVEKIVQGVQLRGRAQGGGALRAPSQG
SGAAARS
```

Signal sequence:

amino acids 1-32

N-glycosylation site.

amino acids 62-66, 96-100, 214-218, 382-386, 409-413, 455-459,
628-632, 669-673, 845-849, 927-931, 939-943, 956-960

Glycosaminoglycan attachment site.

amino acids 826-830

Casein kinase II phosphorylation site.

amino acids 17-21, 39-43, 120-124, 203-207, 254-258, 264-268,
314-318, 323-327, 347-351, 464-468, 548-552, 632-636, 649-653,
671-675, 739-743, 783-787, 803-807, 847-851, 943-947, 958-962,
1013-1017, 1019-1023, 1021-1025

Tyrosine kinase phosphorylation site.

amino acids 607-615

N-myristoylation site.

amino acids 179-185, 197-203, 320-326, 367-373, 453-459, 528-534,
612-618, 623-629, 714-720, 873-879

FIGURE 99

GACGGCTGGCCACC**ATG**CACGGCTCCTGCAGTTTCTGTATGCTTCTGCTGCCGCTACTGCTA
CTGTGTTGGCCACCACAGGCCCGTTGGAGCCCTCACAGATGAGGAGAAACGTTTGATGGT
GGAGCTGCACAACCTCTACCGGGCCAGGTATCCCCAGGCCTCAGACATGCTGCACATGA
GATGGGACGAGGAGCTGGCCGCCTTCGCCAAGGCCACGCACGGCAGTGCGTGTGGGGCCAC
AACAAGGAGCGCGGGCGCCGCGGCGAGAATCTGTTGCCCATCACAGACGAGGGCATGGACGT
GCCGCTGGCCATGGAGGAGTGGCACCACGAGCGTGAGCACTACAACCTCAGCGCCGCCACCT
GCAGCCCAGGCCAGATGTGCGGCCACTACACGAGGTGGTATGGGCCAAGACAGAGAGGATC
GGCTGTGGTTCCCACTTCTGTGAGAAGCTCCAGGGTGTGTAGGAGACCAACATCGAATTACT
GGTGTGCAACTATGAGCCTCCGGGGAACGTGAAGGGGAAACGGCCCTACCAGGAGGGGACTC
CGTGCTCCCAATGTCCCTCTGGCTACCACTGCAAGAAGCTCCCTCTGTGAACCCATCGGAAGC
CCGAAGATGCTCAGGATTTGCCTTACCTGGTAAGTGGGCCCATCCTTCGGGGCGACTGA
AGCATCAGACTCTAGGAAATGGGTACTCCTTCTTCCCTAGCAACGGGGATTCCGGCTTTCT
TGTTAAACAGAGTCTCAGGCTCCCTGGCAACCAAGGCTCTGCCTGCTGTGGAACCCAGGCC
CCAACTTCTTAGCAACGAAAGACCCGCCCTCCATGGCAACAGAGGCTCCACCTTGCGTAAC
AACTGAGGTCCCTTCCATTTTGGCAGCTCACAGCCTGCCCTCCTGGATGAGGAGCCAGTTA
CCTTCCCAAATCGACCCATGTTCTCTATCCAAAATCAGCAGACAAAGTGACAGACAAAACA
AAAGTGCCCTCTAGGAGCCCAGAGAACTCTCTGGACCCCAAGATGTCCCTGACAGGGGAAG
GGAACCTTACCCCATGCCCAGGAGGAGGCTGAGGCTGAGGCTGAGTTGCCCTCCTTCCAGTG
AGGTCTTGGCCTCAGTTTTTCCAGCCCAGGACAAGCCAGGTGAGCTGCAGGCCACACTGGAC
CACACGGGGCACACCTCCTCAAGTCCCTGCCCAATTTCCCAATACCTCTGCCACCCTAA
TGCCACGGGTGGGCGTGCCCTGGCTCTGCAGTCGTCCTTGCCAGGTGCAGAGGGCCCTGACA
AGCCTAGCGTTGTGTGTCAGGGCTGAACTCGGGCCCTGGTCATGTGTGGGGCCCTCTCCTGGGA
CTACTGCTCCTGCCTCCTCTGGTGTGGCTGGAATCTT**TGA**ATGGGATACCACTCAAAGGG
TGAAGAGGTGAGTGTCTCTGTGTCATCTTCCCCACCCTGTCCCCAGCCCTAAACAAGATA
CTTCTTGGTTAAGGCCCTCCGGAAGGGAAAGGCTACGGGGCATGTGCTCATCACACCATCC
ATCCTGGAGGCACAAGGCCTGGCTGGCTGCGAGCTCAGGAGGCCGCTGAGGACTGCACACC
GGGCCACACCTCTCCTGCCCTCCTCCTGAGTCTGGGGGTGGGAGGATTTGAGGGAGCT
CACTGCCTACCTGGCTGGGGCTGTCTGCCACACAGCATGTGCGCTCTCCCTGAGTGCCTG
TGTAGCTGGGGATGGGGATTCTAGGGGCAGATGAAGGACAAGCCCCACTGGAGTGGGGTTC
TTTGTAGTGGGGGAGGCAGGGACGAGGGAAGGAAAGTAACCTCTGACTCTCCAATAAAACCT
GTCCAACCTGTGAAA

FIGURE 100

MHGSCSFLMLLLPLLLLLLVATTGPVGALTDEEKRLMVLEHNLRYAQVSPITASDMLHMRWDEE
LAFAFAKAYARQCVWGHNKERGRGENLFAITDEGMDVPLAMEEWHHEREHYNLSAATCSPGQ
MCGHYTQVVWAKTERIGCGSHFCEKLQGVETNIELLVLCNYEPPGNVKGKRPYQEGTPCSQC
PSGYHCKNSLCEPIGSPEDAQDLPLYLVTEAPSFRAEASDSRKMGTTPSSLATGIPAFILVTEV
SGSLATKALPAVETQAPTSLATKDPPSMATEAPPCVTEVPSILAAHSLPSLDEEPVTFPKS
THVPIPKSADKVTDKTKVPSRSPENSLDPKMSLTGARELLPHAQEEAEAEALPPSSEVLAS
VFPAQDKPGELQATLDHTGHTSSKSLPNFPNTSATANATGGRALALQSSSLPGAEGDPKPSVV
SGLNSGPGHVWGPLLGLLLPLVLGIF

Signal sequence:

amino acids 1-22

N-glycosylation site.

amino acids 114-118, 403-407, 409-413

Glycosaminoglycan attachment site.

amino acids 439-443

Casein kinase II phosphorylation site.

amino acids 29-33, 50-54, 156-160, 195-199, 202-206, 299-303

N-myristoylation site.

amino acids 123-129, 143-149, 152-158, 169-175, 180-186, 231-237,
250-256

Amidation site.

amino acids 82-86, 172-176

Peroxidases proximal heme-ligand signature.

amino acids 287-298

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 1.

amino acids 127-138

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 2.

amino acids 160-172

FIGURE 101

GTAACTGAAGTCAGGCTTTTCATTGGGAAGCCCCCTCAACAGAATTCGGTCATTCTCCAAGTTATGCTGGACGT
 ACTTCTGTGTCTCCCTCTGCTTGCTTTTTTTCACATTAGCAGACCGGACTTAAGTCACAAACAGATTATCTTTTCAT
 CAAGGCAAGTTTCATGAGCCACCTTCAAAGCCTTCGAGAAGTGAACTGAAACCAACATGAATTGGAGACCAATTCC
 AAATCTGGGACCGACTTCGGCAAAATATTACACTTCTCTCCTTGGCTGGAAACAGGATTTGTAATACTACCTCGA
 ACATCTGAAGAGTTTTCAGTCCCTTTGAAACTTTGGACCTTAGCAGCAACAAATATTTACAGAGCTCCAACTGCATT
 TCCAGCCCTACAGCTCAAATATCTGTATCTCAACAGCAACCGAGTCACATCAATGGAACTTGGGTATTTTGACAA
 TTTGGCCAAACACACTCTTTGTGTTAAAGCTGAACAGGAACCGAATCTCAGCTATCCCAACCGAAGATGTTTAAACT
 GCCCACTGCAACACTCTCGAATTGAACCGAACCAAGATTAAATAATGTAGATGGACTGACATTTCCAGGCTTGG
 TGCTCTGAAGTCTCTGAAATGTCGAAAGAAATGGAGTAACGAAACTTATGGATGGAGCTTTTGGGGCTTGAGCA
 CATGGAATTTTCAGCTGGACCTTAACAACTTAACAGAGATTACCAAAGGCTTGGGTTTACGGCTTGCTGTATGCT
 GCAGGAATCTTCACTCAGCCAAAATGCCATCAACAGGATCAGCCTGTAGCTGGAGTCTTGCGGCTTGAGCA
 TGAGCTGGACCTAACTTTCAATCACTTATCAAGGTTAGATGATTCAAGCTTCTTGGCTTAAGCTTACTAAATAC
 ACTGCACATTTGGGAACAACAGAGTCAGCTACATTGCTGATTGGCTTCCGGGGCTTTCAGTTTAAAGACTTT
 GGAATCGAAGAACAAATGAAATTTCTTGGACTATGAAGACATGAATGCTGCTTCTTGGCTTGACAACTGAG
 GCGACTGATCTCCAAGGAAATCGGATCGTCTTATTACTAAAAAGCCTTCACTGGTTGGATGCACTTGGAGCA
 TCTAGCACTGAGTGACACGCAATCATGTCTTTACAAGGCAATGCAATTTTCAAAATGAAGAACTGCAACAAAT
 GCATTTAAATACATCAAGCTTTTGTGGATGTCAGCTACAAATGGCTCCCAAGTGGTGGCGGAAACCACTT
 TCGAGCTTTGTAATGCGAGTTGTGCCCATTCTCAGCTGCTAAAGGAAGAAAGCAATTTTGTGTTAGGCCAGA
 TGAGTTTGTGTGATGATTTTTCCAAACCCAGATCAGGTTCCAGCCAGAAACACAGTCGGCAATTAAGGTTCT
 CAATTTGAGTTTCACTCTGCTCAGCTGCCAGCAGCAGTATTTCCCAATGACTTTTGTGGAAAAAGACCAATGA
 ACTACTGCATGATGCTGAAAGTATGCAAAATATTGCAACAGCTCCCGGCCCAAGGTTGGCGAGGTATGAGGATACCA
 CATCTCTCGCTGCGCGAGGTTGAAATTTGCGAGTGAGGGGAAATATCAGTGTGTCACTTCCAATCACTTTGGTTCT
 ATCTCACTGTCTCAAGCCCAAGCTTACAGTAAATATGCTTCCCTCATTACCAAGACCCCATGGATCTCACCAT
 CCGAGCTGGGSCCATGCGACGCTTGGAGTGTGCTGTGGGGCACCAGCCGCCAGATAGCTGGCAGGAAGA
 TGGGGCCACAGACTTCCAGCTGCAGGGGAGAGACGATGCATGTGATGCCCGAGGATGACGTTGTTTATGCT
 GGAATGAGATAGAGGACATTTGGGTATACAGCTGCACAGCTCAGAAACAGTGCAGGAAGTATTTCAGCAAAATGC
 AACTCTGACTGTCTTGAAGAACCATCATTTTTCGGGCCACTGTTGGACCGAAGTGTAAACCAAGGGAGAAACAGC
 CGTCTCAGAGTCAATGCTGGAGGAAGCCCTCCCTTAACTGAACCTGGACCAAGATGATAGCCCAATTTGTGCT
 AACCGAGAGGCACTTTTTCGAGCAGGCAATCAGCTTCTGATATTGTTGGACTCAGATGTCACTGATGCTGGGAA
 ATACACATGTGAGATGTCTAACACCTTGGCACTGAGAGAGGAAACGTTGGCCTCAGTGTGATCCCCATCCAACT
 CTGGACTCCCTCAGATGACAGGCCCATCGTTAGACGATGACGGATGGGCCACTGTGGGTGTCTGTATCATAGC
 CGTGGTTTGTCTGTGTGTGGGCACTCACTGTGTGGGTGCTCATATATACCAACAGCGGAGGAATGAAGA
 TTGCAGCATTACCAACACAGATGAGACCAATTCGCGACAGATATTTCTAGTTATTGTCACTCAGGGAACGCTT
 AGCTGACAGGCAAGTGGGTACGTGCTTTCAGAAAGTGGAAGCCACCAAGGTTTGCATCACTCAGGTGCTGG
 ATTTTCTTACCAACATGACAGTAGTGGGACCTGCCATATTGACAAATAGCAGTGAAGCTGATGTGGAAGCTGC
 CACAGATCTGCTCTTGTGCTGTTTGGGATCCACAGGCCCTATGTATTTGAAGGAAGTGTGATGCTGGCTCAGA
 TCCCTTTGAAACATATCATACAGTTGCACTCTGACCCAGAAACAGTTTAAATGGACCACTATGAGCCAGTTA
 CATAAAGAAAAAGGAGTGTAACCATGTTCTCATCTCTCAGAAAGATCTCGGCAAGTCTCAGTAAATATATC
 GTGGCCTTCAAGTGTGAGGAAGCTACTTAACTAGTTACTCTCAATGAAGGACCTGGAATGAAATATCTGTG
 TCTAAACAAGTCTCTTTAGATTTTAGTGCAAACTCAGAGCCAGCTCGGTTGCTCGAGTAATCTTTTCATGGG
 TACCTTTGGAAGAGCTCTCAGGAGACCTCAGCTAGATGCTCTATTCAAGCTTTGGACAGCCATCAGATTTGCAGCC
 AAGAGCCTTTTATTTGAAGCTCATTCTTCCAGACTTGGACTCGGTCAGAGGAAGATGGGAAGAAAGGAC
 AGATTTTCAAGGAAGAAATCATTGTTGTTTAAACAGACTTTAGAAACCTCAGAGGACTCCAAATTTTCAGTCT
 TTATGACTTTGGACCACTAGACTGAAATGAGACCAAGGAAAGCTTAACTACTACTCACTCAAGTCAACTTTTATTTA
 AAAGAGAGAAATCTTATGTTTTTTAAATGGAGTTATGAAATTTTAAAGGACATAAAATGCTTTTATATACAGT
 GAACCAAAATTTACAAAAGTATGAAAAATTTTATACCTGGGAATGATGCTCATATAGAATACCTTTTAAACTA
 TTATTTTAACTTTGTTTATGCAAAAAGTATCTTACGTAAATATGATATAAAATCATGATATTTTATGTAATTT
 TTATTAATGCGAGATTTCTTTTATGGAAAAATGAGTTACTAAAGCAATTTAAATAATACCTGCTTGTACCATTTT
 TTAATAGAAGTTACTTCATTATATTTTGCACATTATATTTAATAAAATGTGTCAATTTGAA

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FIGURE 102

MVDVLLLFSLCLLFHISRPLDSHNRLSFIKASSMSHLQSLREVKLNNELETIPNLGPVVSAN
ITLLSLAGNRIVEILPEHLKEFQSLLETLDLSSNNISELQTAFAPALQLKYLYLNSNRVTSMEP
GYFDNLANTLLVLKLNRRNRISAIPKMFKLPLQQLHLELNRRNKIKNVDDLTFQGLGALKSLKM
QRNGVTKLMDGAFWGLSNMBEILQLDHNNLTETITKGWLYGLLMLQELHLSQNAINRISPDWE
FCQKLSLELDLTFNHL SRLDDSSFLGLSLNLTLHIGNNRVSIADCAFRGLSSLKTLDLKNE
ISWTIEDMNGAFSGLDKLRRLILQGNRIRSITKKAFTGLDALEHLDDLSDNAIMSLQGNFASQ
MKKLQQLHLNTSSLLCQDLKWLPLQWVAENNFQSFVNASCAHPQLLKGRSIFAVSPDGFVCD
DFPKPQITVQPETQSAIKGSNL SFICSAASSDSPMTFAWKDNELLHDAEMENYAHRAQG
GEVMEYTTILRLREVEFASEGKYQCVISNHFGSSYSVKAKLTVNMLPSFTKTPMDLIRAGA
MARLECAAVGHPAPQIAWQKDGDTDFPAARERRMHVMPEDDVFFIVDVKIEDIGVYSCTAQN
SAGSISANATLTVLETPSFLRPLLDRTVTKGETAVLQCIAGGSPPKLNWTKDDSPLVVTER
HFFAAGNQLLIIVDSVSDAGKYTCESMNTLCTERGNVRLSVIPTPTCDSPQMTAPSLDDDG
WATVGVIIVAVCCVVGTSVLVVVVIYHTRRRNEDCSITNTDETNPADIPSYLSSQGTLD
RQDGVSSSESGSHHQFVTS SGAGFFLPQHDSSGTCCHIDNSSEADVEAATDLFLCPFLGSTGP
MYLKGNYVSGDPFETHTGSPDPRTVLMDHYEPSYIKKKECYPCSHPSEESCERSFSNISW
PSHVRKLLNTGYSHNEGPGMKNLCLNKSSLD F SANPEPASVASSNSFMGTFGKALRRPHLDA
YSSFGQPSDCQPRAFYLKAHSSPDLD SGSEEDGKERTDFQEENHICTFKQTLENYRTPNFQS
YDLDT

Signal sequence:

amino acids 1-19

Transmembrane domain:

amino acids 746-765

N-glycosylation site.

amino acids 62-66, 96-100, 214-220, 382-386, 409-413, 455-459,
628-632, 669-673, 845-849, 927-931, 939-943, 956-960

Glycosaminoglycan attachment site.

amino acids 826-830

Casein kinase II phosphorylation site.

amino acids 17-21, 39-43, 120-124, 203-207, 254-258, 264-268,
314-318, 323-327, 347-351, 464-468, 548-552, 632-636, 649-653,
671-675, 739-743, 783-787, 803-807, 847-851, 943-947, 958-962,
1013-1017, 1019-1023, 1021-1025

Tyrosine kinase phosphorylation site.

amino acids 607-615

N-myristoylation site.

amino acids 179-185, 197-203, 320-326, 367-373, 453-459, 528-534,
612-618, 623-629, 714-720, 873-879

GGGGAGAGAGGTTGACCACTTAAAGAGGACATTTTTTTTGGTGTTGGTGGCGCTGTGGGTGCTTGCAAAAATG
 AAGGATCGAGGACGACGCTTTCTCTGGACCAAGCAAGGATAAGTAACTGATTGTGCAAGAGAGAGAGCAAGAAC
 GAAGCTTTTCTTTGAGCGCGCTGGATCTTAACAACAAATGTGATGTGATCAATAATAATCTTAAAGCAGTGTCCCTCC
 TAAACCAAGATGACCCGCGGGGTTGGTGTCTTGATCAATAATAATCTTAAAGCAGTGTCCCTCC
 CCACCCCAAAAAGAGATGATTGAAATGAAGACCGAGGATTCACAAAGAAAAGATGTGTCAITTTTCTC
 TAAAGAGAAAGTGTAGCAACAGAGATATTTTGTGAATGAAAGTGTGGGGCTTTTGTAGTAAGTAAAGAACT
 GGTGTGGTGTGTTTCTTCTTTTGTGAATTTCCCAAGAGGAGAGAGAAATAATAATCAATCTGCAAAAGAT
 TTTACAGAAAGAAAGTTGACCGCGCAGATTTGAGGCAATGTGGGGGAGAGAAACACGACAGACAGTTGGTA
 TTTGTGCCATGTGTGACATAAATTCAGGATAATTCAGTTGGATTTTCTTCATCAACCTCTTTTTTTAAAT
 TTTTATCTCTTTGGATATCAAGATCGCTGTTTCTCTGTGTTCAACACCTGGATTTCATCTGTGATGTGTCT
 GTGATCAGTCTGGAATCAACGTGTTGAATTCAGAAGAGCAACACAGATAAATTATGAACTGTGATCAACAGAT
 GACCTTCATCTACACAGACATAATGATAGTGTCTAGGTTTAAACAGGCGCCATTTGACCCCTGCTGTGGTGTCT
 GCTGGCTCTCAACTCTGTGGTGGCTGTGTGGTGGCGCTAGACCTGCCCTCTGTGTGCTCTTGACAGCA
 CCGATTCCAGCAAGTGATTTGTGTTGCGAAAAACCTCGTGAGAGCTCCGGATGGCATCTCCACCAACACCGGCT
 GTGAACCTTCATGAGAACCAATCCAGATCACTAAGGTGAACAGTCTCAAGCATCTGAGGCATTTGAAATCTCT
 ACAGTTGATGAGGAAACCATACGAAACCATGAAATTTGGGGCTTCAATGTTCTTGGGAAACCTCAACATCTGGAA
 ACTCTTGACATCGTCTTACTACATCCGAGATGGAGCTTTGTATGATCTGTCTAAATCTGAGGAGCTCTGTT
 CGGAAACACCCCATGGAAGACCTCCCTTCTTATGCTTTAAACAGATTCCTTTTGGCGCAGTAGACTTAGG
 GGAATGAAGAAAGCTTTCATCATCTCAGAAGTGCTTTGAGAGTCTGCAACTGTGAGTATTGAACTGCTG
 CATGSCACCTTGGGAAGACCTTCACTCTACACCGCTCAATAAAACATGAAGTGTGATCTTTCTGGGAATCA
 TTTATCTGCACTAGCGCTGGCTCTTCCAGGTTTGTAGCATCTTAAAGATGTGGAATGATACGTCAGAT
 TCAAGTGAATGGAAGCAATGCTTTGACAACTCTCAGTCACTAGTGGAGATCAACCTGGGCAACAAATATTAAC
 ATATCTGCTCATGACCTCTCACTCTCTGATCATCTAGACGGATACATTAACATCAACCTCTGGAAGCT
 TAACTGTGATCATCTGTGCTGACGTGTGTGATAAAGAGATGGCCCTCGAACACAGCTGTTGTGGTGGCGGTG
 TAACTCTCCCAATCAAAGGGGAGGTACATTGGAGAGCTGACCAAGATTACTTCATGATCTAGTCTGGT
 GATTGTGGAGCCCCGTGACAGCTGATCTCAAGGCTATGGAGCTGAGGCTGAAATGTGGCGGCTGCATC
 CTGATCATCTGTATCTTGATTACTCAAAATGGAACATCTAGACATGGAGGTACAAGTGGCGATAGTGT
 GCTCATGATGTGATCTTAAATTTCAAAATGTAATCTGTACAGTACAGGCATGTACATGATGTGGTGGATTA
 TTTCCGTTGGGAATCTACTGTTCTCAGCCACCTGAAATGTCTGACGACCAACTACTCTTTCTCTATCTT
 AACCGTCAAGTACAGATTAAGAACGCTCTCAGATGAGGACGCGACAGAGATAAAGTGGGTCCCACTCT
 AGTGTGCGATGGGAGACCACTAATGTGACACCTCTCTACACACAGAGACAAGGTGACAGGGAACCTT
 CACCATCCCACTGATGATAAACAAGTGGATCCAGAGATGTAGAGTTCATGAAGATCAACAAATCATCAT
 TGGGTTTGTGGCCATCACACTCATGCTCGTGTGAGTCTGTGATTTTCAACAGATGAGGAAGCAGCACA
 TCGGCAAAACCATCAGCCCAACAGGATCTTGAATATTAATGTGGATGATGAGTACGGGAGACACAC
 CTGGAAGACCATCTGCCATGCTCTATCTAGAGATGAGCAGCTAAATCTACTAATCATACAACCTTCTCTCT
 CAACCAACCAACACAGTACCAACATAAATCTAAACAACAGTTCAGTGTGATGACCGCTTATTGATCCGATGAA
 CTCTAAAGACAAATGTACAGAGATCTCAATCTTAAACAAATTTACAGATTCACAAAACAAACAATCAAAAAA
 GACGATTTATAAATTAAGACCAAAATGCTGGCTTAATCTACTGTTTCAAAAAGGTGTCTTACAAAAACAA
 AAGAAAGAAAGATTTTATTTATAAAATCTATTGATCTAAGACGACAAAA

FIGURE 104

MLNKMTLHPQQIMIGPRFNRLFDPLLVLALLQLLVVAGLVRAQTCPSVCSCSNQFSKVIC
VRKNLREVPDGI STNTRLLNLHENQIQI IKVNSFKHLRHLEILQLSRNHIRTIEIGAFNGLA
NLNTLELFDNRLTIPNGAFVYLSKLKELWLRNNPIESIPSYAFNRIPSLRRDLGELKRLS
YISGAFEGLSNRLRYLNLAMCNLREIPNLTPLIKLDLDELDSGNHLSAIRPGSFQGLMHLQKL
WMIQSQIQVIERNAPDNLQSLVEINLAHNNLTLLPHDLFTPLHHLERIHLHHNPWNCNDIL
WSWWIKDMAPSNTACCARCNTPPNLKGRYIGELDQNYFTCYAPVIVEPPADLNVTEGMAAE
LKCRASLTSTSVSWITPNGTVMTHGAYKVRIAVLSDGTLNFTNVTVQDTGMYTCMVNSNSVGN
TTASATLNVTAATTPFSYFSTVTVETMEPSQDEARTTDNNVGPTPVVDWETNTVTSLTTPQ
STRSTEKTFITPVTIDINSIGIDVEMKTKIIIGCFVAITLMAAVMLVIFYKMRKQHHRQN
HHAPTRTVEIINVDDEITGDTPMESHLPMPAIEHEHLNHNYSYKSPFNHTTTVTNTINSIHSS
VHEPLLIRMNSKDNVQETQI

Signal sequence:

amino acids 1-44

Transmembrane domain:

amino acids 523-543

N-glycosylation site.

amino acids 278-282, 364-368, 390-394, 412-416, 415-419, 434-438,
442-446, 488-492, 606-610

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 183-187

Casein kinase II phosphorylation site.

amino acids 268-272, 417-421, 465-469, 579-583, 620-624

N-myristoylation site.

amino acids 40-46, 73-79, 118-124, 191-197, 228-234, 237-243,
391-397, 422-428, 433-439, 531-537

[illegible]

AGCGGACGCTGCTCAAGGCGGCAACTCTGTTGCAGTTGGCAGTCTCTTTTCGTTTCCCTCTGCTGTTTGGGGGCA
 TGAAGGCGTTGCGCGCGGAGGTAAAGAAAGGATTTGACCGGGCAGCGGAGGAGAGCGCGCACAGCCGC
 GACCGCGGGGCTGACCCTCGGCTGGAGTTGTTGCGCGGCGCGGAGCGCGCGCGTTGGAGAGTTCCGGTAGA
 CAGCTAGCGCGCTGAGCCGCGATGCGAGCGCGCGAGCTCCGCTGCGCGCGCGGGGTGGGGGCTGCTGTGTCG
 GCGGCTCTGGGCGCGCGTGGCGCTCCAGCGAGCGCGGTGCGGGGAACTCGGCGACCCCTCTGGGGTAGCGCGC
 GAGCGGCCCATGCCCCACTCATCTGCCGCTGCTCGGGGACCTGCTGGACTCGAGTCTAGACCGGTACGCGCTT
 CCGGAGCCCTCCCGTCTGGGTGCGTGGCTGCACTTAAGTACAACAGATTAATCTTTCAACGAGCAAGTCTT
 ATGACGCGCTCTCAAGGCTCTCGAGAAGTGAAATCGAACCAATGAATTTGGAGACATCTTCAAATCTTGGGACCA
 GTCTGCGCAAAATATACACTTCTCTCTTGGCTGGAAAAGAGGATTTGAAATCTCCCTGAACATCTGAAGAAG
 TTTGATGCTCTTGAACATTTGGACTTTAGCAGCAACAATTAATTCAGAGCTCAAATGCTGATTTCCAGGCTCTACAG
 CTCAAATCTGTATTCTCAACGCAACCGAGTCAATCAATGGAACCTGGGTATTTTGAACAATTTGGCCAAACACA
 CTCTCTTGTTTAAAGCTGAACGAGGAACCGAATCTCAGTACTCCACCAAGATGTTTAAATCGGCCCACTGCAAC
 CATCTCGAATTTGAAACCGAAACAAGATTAATAATGTATGATGATGATGACATTCAGAGGCTTGGTGCTTCTGAAGTCT
 TCGAAATATCGAAGAATATGGGATTAACGAAACTTATGATGGAGACTTTTGGGGGCTGAGCAACATGGAATTTTTCG
 CAGCTGACCACTTAAACAACCTAACACAGATTAACAAAGGCTGGCTTTACGGCTTTGCTGATGCTGAGGAACATCA
 CTTCGACCAAAATGCAATCAACAGGATCAGCCCTGATGCTGGGAGTTCTGCGAGAACTCAGTGAAGCTGACCACT
 ACTTTCAATCCTTATCAAGGTTAGATGATTTCAAGTCTCTTGGCTTACGTTACTTAATATCACTGCAATTGGG
 AACCAACGAGTCAAGCTACATGCTGATTTGGCTCTCTCGGGGGCTTTCCAGTTTAAAGAGTTTGGATCTGGAAGAAC
 AATGAATTTCTGCGATGTTTGAAGACATGAATGGTGCTTTCTGCGGCTTGCAAACTGAGGCAAGCTGATCTC
 CAGGAATAATCGATCCGTTCTATTATCAAAAAGGCTCTCATGTTTGGATGCAATGGAGCATCTPAGACCTGAGT
 GACAACGCAATCATGTCTTTACAGGCAATCACTTTTCAAAATGAAGAAGCTGCAACAATGCAATTTAAATACA
 CTAAGCTCTTTGTGCGATGCGCACTAAAATAGCTGCCCAACAGTGGTGCGGGGAAAAGCTTTTCAGAGCTTTGTA
 AATGCGAGTTTGGTCCCATCTCAGCTGTCTAAAGGAGAAGCAATTTTCTGCTTAGCCCAATGGTCTTGTGTTG
 GATGATTTTCCAAAACCCGATACACGCTTCAGCCGAGAAACACAGTGGCAATGAAGAGTTTCCAAATTTGAGTTTC
 ATCTGCTCAGCTGCGCAGCAGTGATTTCCCAATGACTTTTCTGGAAAAGAGCAATGAACTATGCTAGATGAT
 GCTGAATGGGAAAATTTAGTCAACCTCGGGGCCAAGGTGGCGAGGTGATGAGATTAACCAATCTCTTGGCTCT
 CGCGAGGTGGAAATTTGGCAGTGGAGGGAATAATCAGCTGTGTCATCTCCAACTCATTGGTTCATCTACTCTGTC
 AAAGCGCAAGCTCATAGTAATATGCTCTCCCTATCCACGAAGCCCCATGGATCTCAACCTCCGAGCTGGGGGCT
 ATGGACGCTTGGAGTGTGCTGCTGTGGGGCAACGCCGCCCATAGCTGCGAGCAAGATGGGGCGACAGACT
 TCTCCAGCTGCGCGGAGAGCGCATGCTGATGATGCGCGAGGATGACGTGTTCTTTATCTGGATGTGAGATTA
 GAGGACATTTGGGTATTAACGCTGACAGCTCAGAACAGTGCAGGAAGTATTTACAGAAATCGCACTCTGACTGCTC
 CTAGAACAACCAATCATTTTGGGGCAGCTTGGGACGAACTGTAACCCAGGSGAGAAACAGCCGCTGCTACAGTGC
 ATTGCTGGAGGAAGCTCCCTCCCTAACTGAACTGGACAAGAATGATAGCCATTTGGTGTAAACCGAGAGGAC
 TTTTTCGAGCAGGCAACTCAGCTCTGATTAATGTTGGACTCAGATGTCAGTGAATCTGGGAAATACACATTTGAG
 ATGCTTAAACGCTTGGCATGAGAGAGAAACCTGCGGCTCAGATGTATCCCACTCCCACTCGCATCTCCCTCT
 CAGATCAGAGCCCCATCTGTAGAAGCTGACGAGTAGGGCCATCTGGGTGTCGATCATGAGGCTGGGTGGTGTGCT
 GTGTGGGCGAGCTCAGTGTGTGGGTGTCATCATATACACAGCGCGAGGAATGAAGATTTGCGAGTATACC
 AACACAGATGAGCAACCACTTGCAGCAGGATCTTACATTAATGGAACATGAGCGGAGCTTACATAAAGAAAAG
 GAGTGTACCCATGTTCTCATCTCTCAGAGAAGACTCTCGGACAGCGAGTCTGAGATATATATCTGGTGGCTTCACAT
 GTGAGGAGACTCATTAACACTAGTTATATCTCAATGAAGCACTGGAAATGAAAATTTGTTGCTTAAACAAGTCT
 TTTTGTGCTTTTGGGATCCACAGCCCTATCTATTTGAAGGGAATGTTGTGCTCAGATCTTTTGAACA
 TATCATACAGTGTGACTCTGACCCAGCAACAGTTTAAATGGAACATGAGCGGAGCTTACATAAAGAAAAG
 GAGTGTACCCATGTTCTCATCTCTCAGAGAAGACTCTCGGACAGCGAGTCTGAGATATATATCTGGTGGCTTCACAT
 GTGAGGAGACTCATTAACACTAGTTATATCTCAATGAAGCACTGGAAATGAAAATTTGTTGCTTAAACAAGTCT
 TTTTGTGCTTTTGGGATCCACAGCCCTATCTATTTGAAGGGAATGTTGTGCTCAGATCTTTTGAACA
 GCTCTCAGGAGACTCAGCTAGATGCTTATTCAGCTTTTGGACGCACTCAGATTTGAGCAAGCGCTTTTAT
 TGAAGCTCTCATCTCCCGAGCATGGACTCTGGGTGAGGAGAGTGGGAAAGAGGACAGATTTTCAAGAA
 GAAAATCACAATTTGACTTTTAAACAGGCTTTAGAAATACAGACTCCAAATTTTCAGTTCTATGACTTGGAC
 ACATATAGACTGAATGAGGCAAGGAAAGCTTAACTACTACTCAAGTGAAGCTTTTATTTAAAGAGGAGAGAT
 CTATGTTTATTAAGTTGGATTTATGAATTTTAAAGAGGATAAAATGCTTTATTTACAGATGAGCCAAATATAC
 AAAAGTATGAAAATTTTTATCTGGAATAGATGCTCTATAAAGAATACCTTTTAAATATTTTAACTTTGTT
 TTTTATGCAAAAAGTATCTTACGTAAATTAATGATATAAATCATGATTAATTTATGTTATTTATTAATGCGCAT
 TTTCTTTTATGGAATAGTATTAAAGCATTTTAAATATACCTGCTGTCACATTTTATTAATGAGAGTT
 ACTTCATTAATTTTGCAATCTAATTTAAATATGTTCAATTTGAAAAAAAAATAAAAAAAAAAAAAAAAAAAAA

FIGURE 106

MSAPSLRARAAGLGLLLCAVLGRAGRSDSGGRGELQGPSGVAAPERCPCTTCRCLGDLDDCSR
KRLARLPEPLPSWVARLDLSHNRLSFIKASSMSHLQSLREVKLNNELETTINLGPVSPANIT
LLSLAGNRIVEILPEHLKEFQSLETLDLSSNNISELQTAFPALQKLYLNSNRVTSMEBPGY
FDNLANTLLVLKLNRRNRI SAIPPKMFKLQQLQHLELNRRNKIKNV DGLTFQQLGALKSLKMQR
NGVTTKLMDGAFWGLSNMEILQLDHNNTL EITKGWLYGLLMLQELHLHLSQNAINRI SPDAWEFC
QKLSELDLTFNHL SRLDDSSFLGLSLLNTLHIGNNRVSYIADCAFRGLSSSLKTLDLKNNIEIS
WTIEDMNGAFSGLDKLRRLI LQGNRIRSI TKKAPTGLDALEHLDLSDNAIMSLQGNAFSQMK
KLQQLHLNTSSLLCDCQLKWLFPQWVAENNFQSFVNASC AHPQLLKGRSIFAVSPDGFVCDDF
PKPQITVQPETQSAIKGSNLSFICSAASSSDSPMTFAWKKNELLHDAEMENY AHLRAQGG E
VMEYTTILRLREVEFAS EGGKQCVISNHF GSSYSVKAKLTVNM LPSFTKTPMDLTIRAGAMA
RLECAAVGHPAPQIAWQKDG GTDFPAARERRMHVMPEDDVFFIVDVKIEDIGVYSCTAQNSA
GSISANATLTVLETPSFLRPLLDRTVTTKGETAVLQCIAGGSPPPKLNWTKDSDPLVVTERHF
FAAGNQLLII VSDSDVDAGKYTC EMSNTLGTERGNVRLSVIPTPTCDSPQMTAPSLDDD GWA
TVGVVIIAVVCCVVG TSLVWVVI IYHTRRRNEDCSI TNDTETNLPADIPSYLSSQGT LADRQ
DGYVSS ESGSHHQFVTSSGAGFFLPQH DSSGTC HIDNSS EADVEAATDLFLC PFLGSTGPMY
LKGNVYGS DPFETYHTGCSPDPRTVLMDHYEPSYIKKKECYPCHSPSEESCERSFSNISWPS
HVRKLLNTSYSHNEGPMK NLCNLKSSLD F SANPEPASVASSNSFMGTGFKALRRPHLDAYS
SFGQPSDCQPRAFYLKAHSSPDLDSGSEEDGKERTDFQEENHICTFKQTL ENYRTPNFQSYDLDT

Signal sequence:

amino acids 1-27

Transmembrane domain:

amino acids 808-828

N-glycosylation site.

amino acids 122-126, 156-160, 274-278, 442-446, 469-473, 515-519, 688-692, 729-733, 905-909, 987-991, 999-1003, 1016-1020

Glycosaminoglycan attachment site.

amino acids 886-890

Casein kinase II phosphorylation site.

amino acids 99-103, 180-184, 263-267, 314-318, 324-328, 374-378, 383-387, 407-411, 524-528, 608-612, 692-696, 709-713, 731-735, 799-803, 843-847, 863-867, 907-911, 1003-1007, 1018-1022, 1073-1077, 1079-1083, 1081-1085

Tyrosine kinase phosphorylation site.

amino acids 667-675

N-myristoylation site.

amino acids 14-20, 36-42, 239-245, 257-263, 380-386, 427-433, 513-519, 588-594, 672-678, 683-687, 774-780, 933-939

Leucine zipper pattern.

amino acids 58-80, 65-87

FIGURE 107

CAAAACTTGCCTGCGGAGAGCGCCACGCTTGACTTTGAATGGAAGGAGCCCGAGCCCGCGGAGCGCGAGCTGAGAC
TGGGGGAGCGCGTTTCGCGCTGTGGGGCGCCGCTCGGGCGCCGGGGCGCAGCAGGGAAGGGGGAAGCTGTGGTCTGCC
CTGCTCCACGAGGCGCCACTGGTGTGAACCGGGAGAGCCCTGGGTGGTCCCGTCCGCTATCCCTGCTTTATATATA
GAAACCTTCCACACTCGGGAAGGACGCGCGAGGCGAGGAGGGCTCATGGTGAGCAAGGAGGGCGCGCTGATCTGCGAG
GCGCAACGACTTCCGAGTTTACAGATTTTACAGATACCAAAATGGAAGGCGAGGGGAGGAGCAACAGCTTGCCTGGT
TCCATCAGCCTCTGGCGCCCGAGCGCATCTGACTCGGCACCCCTCGAGGACACCTTGGCCAGAGCGGGGTGCTGC
TGCTCTGCTGCTGTGCGGCCACAGCTGCACTGGGACCTGTGCTTGGCGTGAGGGCCCGAGGATTTGGCCGAA
TGTGGGCGCCACGCTGAGCGCCGGAAGAGAAAGAAATTTGCGGAGGAGGAGCGCGGTGCTGTGACTGAGCCCTGAGG
AGCCCGGGCTGCGCCAGCGCGGTGAGCTGCCCCGAGACTGTGCTTCCAGGAGGGCGCTGCTGGAGCTGTG
GCGGTATTGACCTGCGTGAGTTCCCGGGGAGCTGCTGAGCACCAACCACTTATCTCTGAGAAACAAACCGAG
TGGAAAAGATCTAACCCTGAGGAGCTTCCCGGCTGCACCGGCTGGAGACACTGAACTTGCAAAACAAACCGCTGA
CTTCCCGAGGGCTCCGAGAGAAGGCGTTGAGCATCTGACCAACCTCAATTACCTGTACTTGGCCAAATAACAAAGC
TGACCTTGGCACCCCGCTTCTGCGCAACGCGCTGATCAGTGTGGACTTTGCTGCGCAACTATCTCACCAAGATCT
ATGGGCTCACCTTGGCCGAGAAGCAAACCTTGGGTCTGTGTACCTGCACAAACAAAGCTGGCAGACGCGGGG
TGCGGGACAACATGTTCAACGGCTCCAGCAAGCTCGAGGTCTCATCTGTCCAGCAACTTCTGCGCCAGCTGC
CCAAGCACCTGCGCGCTGCCCTGTACAAGCTGCACCTCAAGAAACAAAGCTGGAGAAAGATCCCCCGGGGGCT
TCAGCGAGCTGAGCAGCTGCGCGAGCTATACCTGCAAGAACAACTACCTGACTGACGAGGGCTGGACAACGAGA
CCTTCTGGAAGCTCTCCAGCTGGAGTACCTGGATCTGTCTAGCAACAACTGTCTCGGGTCCAGCTGGGCTGC
CGCGAGCCTGGTGTGCTGCACTTGGAGAAGAACGCCATCGGAGGCTGGAGCGCAATGTGCTGACCCCATCTCC
CGAGCCTGGAGTACCTGTGCTGCACAGCAACCAAGCTGCGGGAGCAGGGCACTCACCCATCGGCTTCCAGGCG
TCAAGCGGTTGCACAGCGGTGCACTTGCACAAACGCGCTGGAGCGGTGCCCATGGCTGCGCTGCGCGGTGC
GCACCTCATGATCTGCTGCACAAACAGATCAGAGGATTTGGCGCGAAGACTTGGCACCACCTACTTCTGGAGG
AGCTCAACCTCAGCTACAAACGCACTCACAGCCCAAGGTGCACCGGAGCGCTTCCGGAAGCTGCGCTGCTGC
GCTCGCTGGACCTGTGCGGCAACCGGCTGCACAGCTGCGCACCCTGGGCTGCTCGAAATGTCCATGTGCTGAAG
TCAAGCGCAATGAGCTGGCTGCTTGGCACGAGGGGCGCTGGCGGGCATGGCTGAGCTGCGTGAAGCTGTACTCTA
CCAGCAACCGACTGCGGACCGGAGCCCTGGGCGCCCGTGCCTGGTGGACTTCCGCACTTGGCAGCTGTGGACA
TCGCGGGAAATCAGCTCAGAGATCCCCGAGGGGCTCCCGGAGTCACTTGAGTACCTGTACCTGCGAGAACAA
AGAATTAGTGGGCTGCGCGGCAATGCTTCCGACTCCAGCGCCAACTCAAGGGGATCTTCTCAGGTTTAAACAAAG
TGGCTGTGGGCTCCGTTGGTGGACAGTGCCTTCCGAGGCTGAAGCACCTCGAGGCTTGGACATTGAAGGCACT
TAGAGTTTGGTGACATTTCCAGGACCGTGGCGCTTGGGGAAGGAAAGGAGGAGGAAGAGGAGGAGGAGG
AGGAAGAGGAAACAGATATGAGCAAGGTGATGAGATGTGACCTAGGATGATGGACCGCGGAGCTTCTTTCTGC
AGCACGCTGTGCTGTGTGAGCCGCCCACTTGGCGGTGCTCACACAGACACCAAGAGCTGCACATGAGGCA
TCCACATGACACGGGCTGACACAGTCTCATATCCCAACCCCTTCCACGGGCGTGTCCACGGCCAGACATGC
ACACACATCACACCCCTCAAAACCCAGCTCAGCCACACAACTACCTTCAAACCACTCAGCTCTCTGTACAC
CCCCACTACCGCTGCCACGCCCTTGAATCATGACGGAAGGGTCTGCCCTGCGCTGGCAACACAGGCAACCA
TTCCCTCCCGCTGATGACATGTGATGTGCTATGCTATGATACACCAACACACACCAAGTCTGCTGCGGA
CAGCCCTCCAAAGCCTATGCCACAGAGCTTGTGCCCGACCCAGAAATCAGCCATAGCAGCTCGCCGTCTGCCCT
GTCCACTGTCCGTCCGCTCCCTCCGAGGAAGACAAAGGATTCATGCTGTGTGGCAGGTGCTGCAACCTCT
GGAATCAACAAAGCTGGCTTTTATCTTTCCATCCTATGGGGAAGGAGCTTCCAGGACTGTGTGGCTGGCC
TGGCCCACTCTCTCCAGGTGCTGGGCACTCACTGTCTAAGAGTCCCTTCCGACCGCCCTGGCAGGAC
CAGGCTGTTTCCAATGGGCAAGCCAGTGGAGGAGGATGGGAGAGCCCTTGGGTGCTGTGTGGGCTTGGG
CAGGAGTAAAGCAGAGGTGATGGGCTGGGCTGAGCCAGGAGGAGGACCCAGCTGCACCTAGGAGACCTTT
GTTCTTCAGGCTGTGGGGGAAGTTCGGGTGCTTATTTTATTTATTTCTTTTAAAGGAAAAATGATAAAAT
CTCAAGCTGATTTTCTGTGTATAGAAAACTAATAAAGCATTTATCCCTATCCTGCAAAAAA

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FIGURE 108

MEGEEAEQPAWFHQWPWPGASDSAPPAGTMAQSRVLLLLLLLLPPQLHLGPVLAVRAPGFGRS
GGHSLSPREENEFAEEEEPVLVLSPEEPGPGPAAVSCPRDCACSQEGVVD CGGIDLREFFPGDLP
EHTNHLSLQNNQLEKIYPEELSRHLRLETLNLQNNRLTSRGLPEKAFEHLTNLNYLYLANNK
LTLAPRFLPNALISVDFAAANYLTKIYGLTFGQKPNLRSVYLHNNKLADAGLPDNMFNGSSNV
EVLILSSNFLRHVPKHLPPALYKLHLKNNKLEKIPPGAFSELSSLRELYLQNNYLTDEGLDN
ETFWKLSSLEYLDLSSNNLSRVPAGLPRSLVLLHLEKNAIRSVLDANVLTPIRSLEYLLHSN
QLREQGIHPLAFQGLKRLHTVHLYNNALERVPSGLPRRVRTLMIHNNQITGIGREDPATTYF
LEELNLSYNRITSPQVHRDAFRKLRLRLSLDLSGNRLHTLPPGLPRNVHVLKVKNELAALA
RGALAGMAQLRELYLTSNRLRSRALGPRAWVDLAHLQLLDIAGNQLTEIPEGLPESLEYLYL
QNNKISAVPANAFDSTPNLKGIFLRFNKLAVGSVVDSAFRRLKHLQVLDIEGNLEFGDISKD
RGRLGKEKEEEEEEEEEETR

Signal sequence:

amino acids 1-48

N-glycosylation site.

amino acids 243-247, 310-314, 328-332, 439-443

Casein kinase II phosphorylation site.

amino acids 68-72, 84-88, 246-250, 292-296, 317-321, 591-595

N-myristoylation site.

amino acids 19-25, 107-113, 213-219, 217-223, 236-242, 335-341,
477-483, 498-502, 539-545, 548-554

Leucine zipper pattern.

amino acids 116-138, 251-273, 258-280, 322-344, 464-486, 471-493,
535-557

FIGURE 109

GGGAGGGGGCTCGGGCGCGCGCAGCAGACCTGCTCCGGCCGCGCGCCTCGCGCTGTCTCTCGGGAGCGGCAG
CAGTAGCCCGGGCGGGCGAGGGCTGGGGGTTCCTCGAGACTCTCAGAGGGGGCGCTCCCATCGGGCGCCACCACCC
CAACCTGTTTCCTCGCGCGCACCTGCGCTGCGCCCGAGGACCGCTGCCAACATGGATTTCCTCTGGCGCTGTT
GCTGGTATCTCTCGCTCTACCTGCAGGCGCGCGCGAGTTCGACGCGGAGGTGGCCAGGCAAAATAGTGTCTATCGAT
TGGCCCTATGTGCTTATGGTGGGAGGATTGACTGCTGCTGGGGCTGGGCTCGCCAGTCTTGGGAGCAGTGTCTAGCC
TGTGTGCCACACAGATGCAAACTGTTGAATGTATCGGGCCAAACAAGTGCAGAGTGTCTCTGGTGTATGTCTGG
AAAAACCTGTAATCAAGATCTAAATAGTGTGGCTGAAGCCCGCGCTCGAAGACAGGTGCATGAACACTTA
CGCGCAGCTACAGTGTCTATGCTCTCAACCGGATATATGCTCATGCCGGATGTTCTCTGCTCAAGTGGCCGTGACCTG
CTCCATGGCAAACTGTGAGTATGGCTGTGATGTTGTTAAAGGACAAATACGGTGGCAGTGCCCATCCCTGGCCCT
GCACCTGGCTCCTGATGGGAGGACCTGTGTAGATGTTGATGAATGTGCTACAGGAAGAGCCCTCTGTCCCTAGATT
TAGGCAATGTGTCAACACTTTTGGGAGCTACATCTGCAAGTGTCTAAAGGCTTCGATCTCATGTATATTGGAGG
CAAAATCAATGTCTGACATAGACGAATGCTCACTTGGTCAGTATCAGTGCAGCAGCTTTGCTCGATGTTATAA
CGTACGTGGTCTTCAAGTGCAAATGTAAAGAAGGATACCGGGTGTATGAGCTGACTTGTGTGTATATCCCAAA
AGTTATGATTGAACCTTCAGGTCCAATTCATGTACCAAGGGGAAATGTTACCATTTTAAAGGGTGACACAGGAAA
CAGGCTACTTCTAAGCCAAACAAGACCTACACCAAGCCCAACCACTTCTTCTCCACCAACCAACCAACCC
CCTGCCAACAGAGCTCAGAACACCTCTACCACTTACAAACCCAGAAAGGCCAACACCGGATGACACTATAGC
ACCAGCTGCCAGTACACCTCCAGGAGGGATACAGTTGACCAACAGGCTACAGACAGACCCCTCAGAAACCCAGAGG
AGATGTGTTTCACTGTTCTGCTACAGTTGTAATTTTGACCAATGACTTTGTGGATGGATCAGGAGAAAGACAA
TGACTTGCACCTGGGAACCAATCAGGACCCAGCAGGTGGACAAATATCTGACAGTGTGGCGACCCAAAGCCCGAGG
GGGAAAAGCTGCACGCTTGGTGTACTCTCTCGCGCCCTCATGCTATTCAGGAGCTGTGCTGTGCTATTGAGGCA
CAAGGTGACGGGGCTGCATCTGCGCACTCCAGGTGTTGTGAGAAAACACGGTGGCCCGCAGGAGCAGCCCTGTG
GGGAAGAAATGGTGGCACTGCTGGAGGCAACACAGATCACTTGGCGGGGCTGACATCAAGAGCGAATCACA
AAGATGATAAAGGGTGGAAAATAAGATCTATGATGAAAATTTAAAGGAACTGGGATATTGAGCTGGAGAAG
AGAAGACTGAGGGGCAACCAATGATGTTTCAAGTATATGAAGGGTGGCAGAGAGGGTGGCGCAACAGCTG
TTCCTCATATGCACTACGAATAGAACAGAGGAAACTGGCTTAGACTAGAGTAAAGGAGCATTTCTTGGCAGG
GGCCATTTGAGATTAAGTCTATAAAAAAAGAGTGTGAAAACTCAGATCTCTCTCTCTTCTTAAAAAATAGAA
TAAAAATTTGCTATTTAAGATGGTTAAAGATGTTCTTACCAAGGAAAAGTAAACAAATATAGAAATTTCCAAA
AGATTTTGTATCTAGTAGTATGCAAGTAAATCTTTAGAACTAAATAATTGGACAAGGCTTAATTATTAGG
CATTTCCCTCTGACCTCTTAATGGAGAGGGATTGAAAGGGGAAGAGCCACCAATGCTGAGCTCACTGAAATA
AGATATTTTAGTATCTCAGTAATGCTTAGTGTGGCGTGGTTTCAATGTTTCTTCA TGGTAAAGGTATAAGCC
TTCCTCCCTTATGGATGATGTTCTTGTCTCGTGTGACAAAGTTATCTTGGCTGTGAGAAAGAGTGGCTGCCCC
ACACCGGCAGACCTTCTCTCACTCATCAGTATGATTGAGTTTCTCTTCAATTTGAGCTCTCCAGGTCTCCAC
AGAACAGTAATATTTTGAACAATAGGTACAATAGAAGTCTTCTGTCAATTTAACCTGGTAAAGAGCAGGCTGAG
AGGGGAAAAATAAATCATTAAGCCTTGAAGTAAACCGCAGAAATATAGGCTGTAGATCAATTTTAAATGGTTTATT
TCCTTTATGTTATATAACTGCACAGTGAAGATGAAAGGGGAAAAATAAATGAAATTTTACTTTTGTATGTTCCAA
TGATACATTTGCACTAACTGATGGAAGAGTTTCAAAAGTACTGTATAACATCTTGTATTATTATTGATGTTT
CTAAAAATAAAATGTTAGTGGTTTCCAAATGGCTTATATAAAACAATTTTGTAAATAAAAAACACTGTTAGTAAAT

GGGAGGGGGCTCGGGCGCGCGCAGCAGACCTGCTCCGGCCGCGCGCCTCGCGCTGTCTCTCGGGAGCGGCAG

FIGURE 110

MDFLLLALVLVSSSLYLQAAAEFDGRWPRQIVSSIGLCRYGGRIDCCWGWARQSWGQCQPVCQP
RCKHGECIGPNKCKCHPGYAGKTCNQDLNECGLKPRPCKHRCMNTVGSYKCYCLNGYMLMPD
GSCSSALTCSMANCQYGCDVVKGQIRQCPSFGLHLAPDGRTCVDVDECATGRASCPRFRQC
VNTFGSYICKCHKGFDLMYIGGKYQCHDIDECSLGQYQCSSFARCYNVVRGSYKCKCKEGYQG
DGLTCVYIPKVMIEPSGPIHVPKGNGTILKGD TGNNNWI PDVGSTWVPPKTPYIPPIITNRP
TSKPTTRPTPKPTPIPTPPPPPLPTELRTPLPPTTPERPTTGLTTIAPAASTPPGGITVDN
RVQTD PQKPRGDFVSVLVHSCNFDHGLCGWIREKDN DLHWEPIRDPAGGQYLTVSAAKAPGG
KAARLVLP LGRMLHSGDCLCSFRHKVTGLHSGTLQVFVRKHGAHGAALWGRNGGHGWRTQI
TLRGADIKSESQR

Signal sequence:

amino acids 1-17

N-glycosylation site.

amino acids 273-277

Casein kinase II phosphorylation site.

amino acids 166-170, 345-349

Tyrosine kinase phosphorylation site.

amino acids 199-206

N-myristoylation site.

amino acids 109-115, 125-131, 147-153, 191-197, 221-227, 236-242,
421-427, 433-439, 462-468, 476-482

Aspartic acid and asparagine hydroxylation site.

amino acids 104-116, 186-198, 231-243

Cell attachment sequence.

amino acids 382-385

EGF-like domain cysteine pattern signature.

amino acids 75-87

Year	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099
1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	

CTTCTTTGAAAAGGATTTATCACCTGATCAGGTCCTCTCTGCATTGGCCCCTAGATTGTGA
AATGTGGCTCAAGGTTCTTCAACAATTTCTCTTTCTTGGCAACAGGTGCTTCTCGGGGCTGA
AGGTGCAGTGGCCATCACACATGTCTACCTGGCGTCAGAGTGAGGCCCTCTACCTACCGCTG
CACTATGGCTTCCACATCTCAGCATCACAGATCAGATCATATGGCTATTTTGAGAGACCCCA
CACAATGGCCCAAATACTTACTTGGGGCTCTGTGAATAAGTCTTGGTCTTCTGACTTGGGAATC
AACACAAGTTTACCAGTGATGCCACCAATGCATCTCTGCTTATCAACCCCATCGAGTTCCC
GATGAGGCAATTCATCTGTGAAGGTCAACATTCACGGGAATGGAACTCTATCTGCCGATCA
GAAGATACAAGTCACGGTTGATGATCTCTGCACAAAGCCAGTGGTGAGAACTCATCTCCCT
CTGGGGCTGTGGAGTATGTGGGGAACATGACCCTGCATGCCATGTGGAAGGGGGCACTCGG
CTAGCTTACCAATGGCTAAAAAATGGGAGACTGTCCACACAGGACTCCACCTACTCTCTTTTC
TCCCCAAAACAAATACCTTTATATTTGCTCTCAGTAACCAAGGAACATTTGGAAATTTACAGCT
GCGCTGTGAGGAACCCCTGTCAGTGAATGAAAGTGATATCATATGCGCCATCATATATTAT
GGACCTTGTGACTTCAAGTGAATTCGATAAAGGCCATAAAGTAGGGGAAGTGTTACTGT
TGACCTTGAGAGGCCATCTATTTGATTGTTTCTGCTGATTTCTATCCCCCAACACCTACT
CTCGGATTAGGAGGATCAACAATATCATATATCATTAAGCATGGGCTCGCTTGAAGTTT
GCATCTGAAAGGTAGGCCAGAAGACATGGACTATGTGTGCTGTGCTTACCAACAACATAAC
CGGCAGGCCAAGATGAACATCATTTACAGCTTATCATCATCTCCGTAGGACCTGGAGAAAGCTTG
CACAGAAAGGAAATCATTTGTCACTTTAGCAAGTATAAATGGAATATCACTATTTTGATT
ATATCCATGTGTCTTCTCTTATGTGAAAAAATATCAACCTCAAAAGTTATAAAACAGAA
ACTGAAAGGCAGGCCAGAAACAGAATACAGGAAGCTCAAAACATTTTCAGGCCATGAAGATG
CTCTGGATGACTTTCGGAATATGAATTTGTCTTTCCAGATGTTTCTGTGTTCTCCAGG
ATTCCAAGCAGGTCGTGTCCAGCCTCTGATTGTGTATCGGGCAAGATTTGCACAGTACAGT
GTATGAAGTTATTACGCACATCTCCGCCAGCAGCAAGCATCCAGATGGAATCTTATCTGG
CTAAACAGCATCATTCGATGAAATTTCTGAAGAAACATTTTAAAGGAAAAACAGTGGAAAGT
ATATTAATCTGGAATCAGTGAAGAAACAGGACCAACACCTTTACTCATTTATCTCTTTACA
TGCAAGATAGAGCATTTATGCAAAATGAATCCAGGTTTTTTCAGCATATACAAGTTCTTCT
GTGCAACAGAAACAAATCTGTGGGGAAATATTTCTCAGTGGAGAGTCGTTCTCATGCTGACGG
GGAGAACGAAAGTGACAGGGGTTTCCCTACAAGTTTGTGTATGAAATATCTCTACCAACCTCA
ATTAGTTTCTACTCTACATCTTTCTCATCATCAAGCTGAGACATCTGTCTTCACTACAA
TGTGGAAACCTTTACATTTGTCGATTTTTCAGCAGACTTGTGTTTTATTAATTTTTTATTAGT
TTAAGATGCTAAATTTATGTTTCAATTTTATTTTCAAAATTTCTATCTGTTATTTGTACA
CAAAGTAATAAGGATGTTGTGCACAAAAACAAATGATGCTTCTCTTTTTTTTCAATCACC
AGTATGATTTTGTGAAGACTGTGGAACATCTAAGGAATAGCATTTAAAGCTCTTATTTTA
TTTTTTTCAAGGAAGATGGATTCAAATAATTTCTGTTTTTGTCTTTTAAAAAATAAAAAA

FIGURE 112

MWLKVFTTFLSFATGACSGLKVTVPSTVHGVGRGQALYLPVHYGFHTPASDIQIIWLFERPH
TMPKYLLGSVNKSVVPDLEYQHKFTMMPPNASLLINPLQFPDEGNIVKVNIIQNGTSLASQ
KIQVTVDDPVTKPVVQIHPPSGAVEYVGNMTLTCHVEGGTRLAYQWLKNGRPVHTSSYSFS
PQNTLHIAPVTKEDIGNYSCLVRNPVSEMESDIIMPIIYYGPGYGLQVNSDKGLKVGEVFTV
DLGEAILFDCSADSHPPNTYSWIRRTDNTTYIIKHGPRLEVASEKVAQKTM DYVCCAYNNIT
GRQDETHFTVIITSVGLEKLAQKGKSLSPASITGISLFLIISMCLLFLWKKYQPYKVIKQK
LEGRPETEYRKAQTFSGHEDALDDFGIYEFVAFPDVSGVSRIPSRSPASDCVSGQDLHSTV
YEVIQHIPAQQQDHPE

Signal sequence:

amino acids 1-18

Transmembrane domain:

amino acids 341-359

N-glycosylation site.

amino acids 73-77, 92-96, 117-121, 153-157, 189-193, 204-208,
276-280, 308-312

Casein kinase II phosphorylation site.

amino acids 129-133, 198-202, 214-218, 388-392, 426-430, 433-437

Tyrosine kinase phosphorylation site.

amino acids 272-280

N-myristoylation site.

amino acids 15-21, 19-25, 118-124, 163-167, 203-209, 231-237,
239-245

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

FIGURE 113

GCAAGCGGCGAAATGCGGCCCTCCGGGAGTCTTGCAGTTCCCCTGGCAGTCTCTGGTGCTGTT
GCTTTGGGGTGCTCCCTGGAGCGCACGGGCGGGAGCAACGTTTCGCCTCATCACGGACGAGA
ACTGGAGAGAACTGCTGGAAGGAGACTGGATGATAGAATTTTATGCCCCGTGGTGCCCTGCT
TGTCAAAACTCTTCAACCGGAATGGGAAAGTTTGTCTGAATGGGGAGAAGATCTTGAGGTTAA
TATTGCGAAAGTAGATGTCACAGAGCAGCCAGGACTGAGTGGACGGTTTATCATAACTGCTC
TTCCTACTATTTATCATTTGTAAGATGGTGAATTTAGGCGCTATCAGGGTCCAAGGACTAAG
AAGGACTTCATAAACTTTATAAGTGATAAAGAGTGAAGAGTATTGAGCCCGTTTCATCATG
GTTTGGTCCAGGTTCTGTTCTGATGAGTAGTATGTCAGCACTCTTTCAGCTATCTATGTGGA
TCAGGACGTGCCATAACTACTTTTATGAAGACCTTGGATTGCCAGTGTGGGGATCATATACT
GTTTTTGCTTTAGCAACTCTGTTTTCGGGACTGTTATTAGGACTCTGTATGATATTTGTGGC
AGATTGCCCTTGTCTTCAAAAAGCGCGCAGACCACAGCCATACCCATACCCCTTCAAAAAAT
TATTATCAGAATCTGCACAACCTTTGAAAAAAGTGGAGGAGGAACAAGAGGCGGATGAAGAA
GATGTTTCAGAAGAAAGCTGAAAGTAAAGAAAGGAACAACAAGACTTTCCACAGAATGC
CATAAGACAACGCTCTCTGGGTCCATCATTTGGCCACAGATAAAATCCTagTTAAATTTTATAG
TTATCTTAATATTATGATTTTGATAAAACAGAAGATTGATCATTTTGTTTGGTTTGAAGTG
AACTGTGACTTTTTTGAATATTGCAGGGTTCAGTCTAGATTGTCATTAAATTTGAAGAGTCTA
CATTCAGAACATAAAAGCACTAGGTATACAAGTTTGAAATATGATTTAAGCACAGTATGATG
GTTTAAATAGTTCTCTAATTTTGAAAAATCGTGCCAAGCAATAAGATTTATGTATATTGT
TTAATAATAACCTAATTTCAAGTCTGAGTTTGAAAAATTTACATTTCCCAAGTATTGCAATTAT
TGAGGTATTTAAGAAGATTATTTTAGAGAAAAATATTTCTCATTGTATATAATTTTCTCTG
TTTCACTGTGTGAAAAAAGAAGATATTTCCATAAATGGGAAGTTTGCCCATTTGTCTCAAG
AAATGTGTATTTCAGTGACATTTCTGTGTTCTTTTAGAGGTATATCCAAAATTTCTTGT
ATTTTATAGTTATGCACTAATAAAACCTACCTTACATTAATTAATTACAGTTTTCTACACA
TGGAATACAGGATATGCTACTGATTTAGGAAGTTTAAAGTTTCATGGTATTCTCTTGATTC
CAACAAAGTTTGATTTTCTCTGTATTTTCTTACTTACTATGGGTTACATTTTATTTT
CAAAATTTGGATGATAATTTCTTGGAAACATTTTATATGTTTATGTAACAGTATTTTGTGTT
GTTTCAAACTGAAGTTTACTGAGAGATCCATCAAAATGAACAACTCTGTGTGAATTTAAAT
TTGGCCACTTTTTCAGATTTTACATCATTCTTGCTGAACCTTCAACTTGAAATTGTTTTTT
TTTCTTTTGGATGTGAAGGTGAACATTCTCTGATTTTGTCTGATGTGAAAAAGCCTTGGTA
TTTTACATTTTGAAAAATCAAAAGAGCTTAATATAAAAGTTTGCACTTCTACAGGAAAAAG
CATCTTCTGTATATGTCTTAAATGTATTTTGTCTCATATACAGAAAGTTCTTAATGTAT
TTTACAGTCTGAATGCTTGTATGTTTTAAATAATAACATTTTATATTTTTTAAAGACAA
ACTTCATATTATCCTGTGTTCTTCTGACTGGTAATATTGTGTGGGATTTACAGGTA
GTCAGTAGGATGGAACATTTTAGTGATTTTACTCCTTAAAGAGCTAGAATACATAGTTTT
CACCTTAAAGAAAGGGGAAAAATCATAAATACAATGAATCAACTGACCAATCAGTAGTAGAC
AATTTCTGAATGTCCCTTCTTCTTAGGCTCTGTGCTGTGTGAATCCATAGATTTACAG
TATCATAATACAAAGTTTCTTTAAAGCCCTCTCTTTAGAATTTTAAATTTGTACATT
AAAGAGTTTGGATGTGTAACCTGTGATGCCTTAGAAAAATATCCTAAGCACAAAATAAACCT
TTCTAACCACTTCATTAAAGCTGAAAAAATAAATAAATAA

FIGURE 114

MAPSGSLAVPLAVLVLLWGPWTHGRRSNVRVITDENWRELLEGDWMIEFYAPWCPACQNL
QPEWESFAEWGEDLEVNIKVDVTEQPGLSGRFIITALPTIYHCKDGEFRRYQGPRTKKDFI
NFIKDKEWKSIEPVSSWFGPGSVLMSSMSALFQLSMWIRTCHNYFIEDLGLFPVWGSYTVFAL
ATLFSGLLLGLCMIFVADCLCPSKRRRPQYPYPYPSKLLSESAQPLKKVEEEQEADEEDVSE
EEAESKEGTNKDFPPQNAIRQPSLGPSTDKS

Signal sequence:

amino acids 1-26

Transmembrane domain:

amino acids 182-201

Casein kinase II phosphorylation site.

amino acids 68-72, 119-123, 128-132, 247-251, 257-261

Tyrosine kinase phosphorylation site.

amino acids 107-115

N-myristoylation site.

amino acids 20-26, 192-198

Amidation site.

amino acids 25-29

FIGURE 115

GCAGTGTCCAGCTGCGGAGACCCGTGATAATTCGTAACTAATTCACAAACGGGACCTT
CTGTGTGCCAGAAACCCGAAGCAGTTGCTAACCCAGTGGGACAGGCGGATTGGAAGAGCGGG
AAGGTCCTGGCCGAGAGCAGTGTGACACTTCCCTCTGTGACCATGAAACTCTGGGTGTCTGC
ATTGTCTGATGGCCCTGGTTTGGTGTCTTGAGCTGTGTGCAGGCCGAATTCCTCACCTCTATTG
GGCACATGACTGACCTGATTTATGCAGAGAAAGAGCTGGTGCCAGTCTCTGAAAGAGTACATC
CTTGTGGAGGAAGCCAGCTTTCCAAGATTAAAGAGCTGGGCCAACAAATGGAAGCTTGAC
TAGCAAGTCAGCTGCTGATGCTGAGGGCTACCTGGCTCACCTGTGAATGCCTACAAACTGG
TGAAGCGGCTAAACACAGACTGGCTTGCCTGGAGGACCTTGTCTGTGAGGACTCAGCTGCA
GGTTTTTATCGCCAAACCTCTCTGTGCAGCGGCAGTTCTTCCCACTGATGAGGACGAGATAGG
AGCTGCCAAAGCCCTGATGAGACTTCAGGACACATACAGGCTGGACCCAGGCACAATTTCCA
GAGGGGAACCTTCCAGGAACCAAGTACCAGGCAATGCTGAGTGTGGATGACTGCTTTGGGATG
GGCCGCTCGGCCATAATGAAGGGGACTATTATCATACCGTGTGTGGATGGAGCAGGTGCT
AAAGCAGCTTGATGCCGGGGAGGAGGCCACCACAACCAAGTCACAGGTGCTGGACTACCTCA
GCTATGCTGTCTTCCAGTTGGGTGATCTGCACCGTGCCCTGGAGCTCACCCGCGCTGCTC
TCCCTTGACCCAAGCCACGAACGAGCTGGAGGGAATCTGCGGTACTTTGAGCAGTTATTGGA
GGAAGAGAGAGAAAAACGTTAAACAAATCAGACAGAAGCTGAGCTAGCAACCCAGAAAGGCA
TCTATGAGAGGCCCTGTGGACTACCTGCCTGAGAGGGATGTTTACGAGAGCCCTCTGTCTGGG
GAGGGTGTCAAAC TGACACCCCGTAGACAGAAGAGGCTTTTCTGTAGGTACCACTTGGCAA
CAGGGCCCAACAGCTGTCTATTGCCCCCTTCAAAGAGGAGGACGAGTGGGACAGCCCGCAC
TCGTCAAGTACTACGATGTCTATGCTGTGATGAGGAAATCGAGAGGATCAAGGAGATCGCAAAA
CCTAAACTTGACAGAGCCACCGTTCTGTGATCCCAAGACAGGAGTCCCTCACTGTCTGCAGCTA
CCGGGTTTCCAAAAGCTCTGGCTAGAGGAAGATGATGACCCTGTGTGTGGCCCGAGTAAATC
GTCCGATGCAGCATATCACAGGGTTAACAGTAAAGACTGCAGAATTGTTACAGGTTGCAAAAT
TATGGAGTGGGAGGACAGTATGAACCGCACTTCGACTTCTCTAGGCGACCTTTTGACAGCGG
CCTCAAAAACAGAGGGGAATAGGTTAGCGACGTTTCTTAACTACATGAGTGATGTAGAAGCTG
GTGTGTGCCACCGTCTTCCCTGATCTGGGGGCTGCAATTTGGCCTAAGAAGGGTACAGCTGTG
TTCTGGTACAACCTCTTGGGAGCGGGGAAGGTGACTACCGAAACAAGACATGCTGCCTGCC
TGTGCTTGTGGGCTGCAAGTGGGTCTCCAATAAGTGGTCCATGAACGAGGACAGGAGTTCT
TGAGACCTTGTGGATCAACAGAAGTTGACTGACATCCTTTTCTGTCTTCCCTTCTCTGGTCT
CTTCAGCCCATGTCAACGTGACAGACACCTTTGTATGTTCTTTGTATGTTCTTATCAGGCT
GATTTTTGGAGAAATGAATGTTTGTCTGGAGCAGAGGGAGACCATACTAGGGCGACTCCTGT
GTGACTGAAGTCCCAGCCCTTCCATTACGCTGTGCCATCCCTGGCCCCAAGGCTAGGATCA
AAGTGGCTGCAGCAGAGTTAGCTGTCTAGCGCTAGCAAGGTGCCTTTGTACCTCAGGTGTT
TFAGGTGTGAGATGTTTTCAGTGAACCAAGTTCTGATACCTTGTTTACATGTTTGTTTTAT
GGCATTTCTATCTATTGTGGCTTTACCAAAAAATAAAATGTCCCTACCAAGAAAAAAA

FIGURE 116

MKLWVSALLMAWFGVLSCVQAEFFTSIGHMTDLIYA EKELVQSLKEYILVEEAKLSKIKSWA
NKMEALTSKSAADAEGYLAHPVNAYKLVKRLNTDWPAL EDLVLDQSAAGFIANLSVQRQFFP
TDEDEIGA AKALMRLQDTYRLDPGTISRGE LPGTKYQAMLSVDDCFGMGRSAYNEGDDYHTV
LWMEQVLKQLDAGEEATTTKSQVLDYLSYAVFQLGDLHRALELTRRLSLDPSHERAGGNLR
YFEQLLEEEREKRLTNQTEAELATPEGIYERPV DYLPERDVYESLCRGE GVKLTPRRQKRLF
CRYHHGNRAPQLLIAPFKEEEDWDSPHIVRYD VMSDEEIERIKEIAKPKLARATVRDPKTG
VLTVASYRVSKSSWLEEDDDPVVARVNR RMQHITGLTVKTAE LLQVANYGVGGQYEPHFDFS
RRPFD SGLKTEGNRLATFLNYMSDVEAGGATVFPDLGAAIWPKKGTAVFWYNLLRS GEGDYR
TRHAACPVLVGCKWVSNKWFHERGQEFLRPCGSTEVD

Signal sequence:

amino acids 1-17

N-glycosylation site.

amino acids 115-119, 264-268

Glycosaminoglycan attachment site.

amino acids 490-494

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 477-481

Casein kinase II phosphorylation site.

amino acids 43-47, 72-76, 125-129, 151-155, 165-169, 266-270,

346-350, 365-369, 385-389, 457-461, 530-534

Tyrosine kinase phosphorylation site.

amino acids 71-80, 489-496

N-myristoylation site.

amino acids 14-20, 131-137, 171-177, 446-452

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 8-19

Leucine zipper pattern.

amino acids 213-235

[illegible]

GCAATATTAGATTTACTACTCTCTCTTTTAGTGGGAAGACAGACCAATATCCAGTGTGAGTGAATTTGATGT
TCTATTATTACCGTTTGTGGCTGGGGGTAGTTCTGCACACCTTCACAGTTAGAGAGCAGGCAAGAAGGATTTGGA
AGACAGGACAATCTCTTGGGATGCTGTCTGGAGACAGCGGGCCCTTGCTGCTCTTTGGCCTATTGACCC
CAGGTTCTCTGTGTTAAACTAGAAAGCTACTCTGCCTGGTGCCCATCAATCTCAAGTGTCTTGTAGGCTGTGCC
CTTGGGACCCACCTCGAGGGGCTACACCTAGTCAGCTAGCTCCCTTTGGCTCTGCTGGGCCAGGCGTCT
CCCTCACTTTAGGCGTGTCTCTGGGGTGCAGCTGTAGCTCTCTGGGGTTTCTGGATCAGGGGGGGGGAAG
ATCCCTGTGTGAGAGCTGTAGGGAGCAGAGAGGGCCACAGAACTCAGATTGAGAGCTCGGTAGACCAAGAT
ATGAAGACTTCAAAACCCGGATTTCCCTCTATACAGGAGGCCCAACAGGCTCTACAGAAGAGGTGCTCAGAGCT
GTGATCATCAGACAGAGCTGGGCTCGGCTGAGCGGTTGCTGGTGGTCTGTCTGACCTCCGAGCTACACTGTCCA
CTTGTCCGGTGGTGTGAACCTGTACGTTGCCCATCACTTCTCGGTGTATCTCTATCTAGGCGAGCGGGGG
CCGGGCTCCAGGAGGATCAGGTGTGTCTCATGGGATGAGGCGCCGCTGGCTCATGTACAGACACCTGC
GCCACTTACACACATCTTTGGGCGCACTACAGTGTGTTTTCATCATCAGAGATGACACATATGTGACAGCCC
CCCGCTGTGCAGCCTTGTGTGCCCACTCAGACTCAACCAAGACCTGTACTAGGCCGAGCAGAGAGTTCATGT
GCGCAGGCGAGCGGCCGTGATCTATGCGGCTTTGGCTACCTGTCTGCTCATCGGAGTCTCTGCTCTGTCTGCG
GGCCACTCTGTGATGGCTCGGAGAGACATCTCAGTGGCCGCTGTGACAGTGGCTTGGACCGTCCCTATTG
ACTCTCTGGGCTGGGCTGTGTCTACAGACACAGGCGCAGCATGTATGCTCAATTTGAAGCTGGCCAAATATAGGG
ACCTCGAGAGAGGAGGAGCTCGGCTTTCTGAGTGCCCTTCGCGCTGACCTGTCTCGAAGGTACCCCTATGT
ACCGGCTCCACAAACGCTCTCAGGCTCTGAGGTTGGAGCGGGCTGTACAGTAATATGAGCAACTGCGACCTCAGA
TCCGGAACCTGACCGTGTCTGACCCCGCAAGGGGAGCAGGGCTGAGCTGGCCCGTTGGGCTCCCTGCTCTTTTCA
CACCACACTCTCTCTTTGAGGTGTGGGCTGGGACTCTACAGAGCAGACACCTTTCTCTGTGAGATGGG
ATCCGCAAGTCCCACTACAGGGGCTAGCAGGGCGAGCAGTGTGTATGCTTTGAGATCGCTCCCTGGAGCAGCTCA
CTCGGCGTCCAGTCCAGCCCGCTCGGCTTCAGAGACGACGATCTACACCGGTATCGGCGCTCTGCACCAGAC
GGGATCGAGTATGAGTATCACCCTGGACCTGCTTTTGAATGTTGTGACACAGCTGGGCAACCGCGGGCCCTGGCTGCA
GGTCAAGCTCTCTGGCCACATGAGCGGGTGGAAATCTAACTATGTGCCATTGTCACTGAGGCCACCGGATGCG
AGCTGSTGTCTGCACCTCTGTTGGTGTGAAGTCTGAAGCTCCCGGCTTTCTCGAGGCTTTGTGACGCAATGTCTC
TGAGGACACGAACTATGATGCTCACTCTGTGCTGGTCTACGGGCAAGAGAGGTGGCCGTGGAGTCTGAC
ACCCATTTCTTGGGTTGAGGCTCGACAGCGGATGTAGAGGACAGGTTACCGTGGACAGGCTGGCTCTGCTCTG
CTGTGCGAGCAGGAGGCCCTTCCAGGTTGCGACTCATGGAGCTGTCTGAAAGAGACACCTGTGACACTCTCT
TCTTCTTACCAACCTGTGGAACAGGCTGGGCGCGAAGTCTCAACCGCTGTGCGATGAATGACCTCTGTGCT
GGAGGCTCTTCTTCAAGTGTGATTCAGAGGATTCAACTTGCCTGCTGTACACAGAGATACCCCGAGGCCCC
CGGGGCTGTGGCCCTGACCCCTCTCCCTCTCTGTTGTGACCCCTCCGGGGGGCTCTTATAGGGGGGAGATTTC
ACCGCAGGCTTTCTGGGAGGGCTGTCTTACAAACGCTGACTACTGCGCGCGCGAGCCGCTGGCAGTGAATG
TGCGAGCGGCAAGAGAGAGAGGCCCTGTGGGGGCTGGAGTGTATGATGTTTCTCCGCTTCTCAGGCTTC
ACCTCTTTTCGGGCGGTAGGACAGGCTGTGTGACAGATCTCCCTCGGACATCTGACCCCGCTCAGGCTGAG
AACTCTACCAACCGCTGGCCCTCGACAACTGAGAGAGGCTGAGGGGCGTCCGACAGCTGTGATAGGCTCTTTG
AGCAGGAGGACGCCATAGCACTTAGCGGCTAGGGGCGCTAACTCACTTCTTCTTGTCTGCCCTCAGCC
CGAGGAAGGCGACGCAAGATGGTGGACAGATAGAGAAATGTTGTGCTATTTTAAATATGAAATTTGTTATTAT
ACATGTTCTTCTGCG

FIGURE 118

MRLSSLLALLRPALPLIILGLSLGCSLSLLRVSWIQEGEDPCVEAVGERGGPQNPDSSRARLD
QSEDEDKPKRIVPYRDPNPKYKKVLRTRYIQTELGSRERLLVAVLTSRATLSTLAVAVNRTV
AHHFPRLLYFTGQRGARAPAGMQVVSHGDERPAWLMSSETLRHLHTHFGADYDWWFFIMQDDTY
VQAPRLAALAGHLSINQDLYLGRAEEFIGAGEQARYCHGGFGYLLSRSLLLRLRPHLDGCRG
DILSARPDDEWLGRCLIDSLGVGCVSQHQGQQYRSFELAKNRDPEKEGSSAFLSAFAVHPVSE
GTLMYRLHKRFSALELERAYSEIEQLQAQIRNLTVLTPEGEAGLSWVPGLPAPFTPHSRFEV
LGWDYFTEQHTFSCADGAPKCPLOGASRADVGDALETALEQLNRRYQPRLRFPQKQRLNLNGYR
RFPDPARGMEYTLDDLLLECVCVQRGHRRALARRVSLRLPLSRVEILPMPYVTEATRVLVPLL
VAEAAAAPAFLEAFAANVLEPREHALLTLLLVYGPREGGRGAPDPFLGVKAAAELERRYPG
TRLAWLAVRAEAPSQVRLMDVVSKKHFPVDTLFFLTVTWTRPGPEVLNRCRMNAISGWQAFFP
VHFQEFNPALSPQSRPPGPPGAGDPDPPSPPGADPSRGAPIGGRFDRQASAEBCFYNADYLAA
RARLAGELAGQEEEEALEGLEVMDFLRFSGHLHFRAVEPGLVKQKFSLRDCSPRLSEELYHR
CRLSNLEGLGGRAQLAMALFEQEANST

Signal sequence:

amino acids 1-15

Transmembrane domain:

amino acids 489-507

N-glycosylation site.

amino acids 121-125, 342-346

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 319-323, 464-468

Casein kinase II phosphorylation site.

amino acids 64-68, 150-154, 322-326, 331-337, 368-372, 385-389,
399-403, 409-413, 473-477, 729-733, 748-752

Tyrosine kinase phosphorylation site.

amino acids 736-743

N-myristoylation site.

amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550,
558-564, 651-657, 657-663, 672-678

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 14-25

Cell attachment sequence.

amino acids 247-250

FIGURE 119

CGGAGTGGTGCGCCAACGTGAGAGGAAACCCGTGCGCGGCTGCGCTTTCCTGTCCCAAGCC
GTTCTAGACGCGGGAAAAATGCTTTCTGAAAGCAGCTCCTTTTTGAAGGGTGTGATGCTTGG
AAGCATTTTTCTGTCTTTGATCACTATGCTAGGACACATTAGGATTTGGTCATGGAAATAGAA
TGCACCACCATGAGCATCATCACCTACAAGCTCCTAACAAAGAAGATATCTTGAAAAATTTCA
GAGGATGAGCGCATGGAGCTCAGTAAGAGCTTTGAGTATACTGTATTATCCTTGTAAGAAC
CAAAGATGTGAGTCTTTGGGCTGCAGTAAAGGAGACTTGGACCAAACACTGTGACAAAGCAG
AGTTCTTCAGTCTGAAAAATGTTAAAGTGTGAGTCAATTAATATGGACACAAATGACATG
TGGTTAATGATGAGAAAAAGCTTACAAATACGCCCTTTGATAAGTATAGAGACCAATACAATG
GTCTTTCCTTGCACGCCCACTACGTTTGCTATCATTGAAAACCTAAAGTATTTTTGTAA
AAAAGGATCCATCAGAGCTTTCTATCTAGGCCACACTATAAAATCTGGAGACCTTGAATAT
GTGGGTATGGAAGGAGGAATGTCTTAAGTGTAGAATCAATGAAAAGACTTAAACAGCCTTCT
CAATATCCCAGAAAAGTGTCTGAACAGGGAGGGATGATTTGGAAGATATCTGAAGATAAAC
AGCTAGCAGTTTGCTGAAATATGCTGGAGTATTTGCAGAAAATGCAGAAGATGCTGATGGA
AAAGATGATTTAATACCAAATCTGTTGGGCTTTCTATTAAAGAGGCAATGACTTATCACC
CAACCAGGTAGTAGAAGCTGTTGTTGAGATATGGCTGTTACTTTTAATGGACTGACTCCAA
ATCAGATGCATGTGATGATGTATGGGGTATACCGCCTTAGGGCATTGCGGCATATTTCAAT
GATGCATTGTTTTCTTACCTCCAAATGGTTCTGACAATGACTGGAAGTGGTAGAAAAGCG
TGAATATGATCTTTGTATAGGACGTGTGTTGTCAATTATTGTAGTAGTAACATACATATCCAA
TACAGCTGTATGTTCTTTTTCTTTCTAATTTGGTGGCACTGGTATAACCAACACATTAAAG
TCAGTAGTACATTTTAAATGAGGGTGGTTTTTTCTTTTAAACACATGAACATTGTAATG
TGTGGAAGAAGTGTTTTAAAGAATAATAATTTGCAAATAAACTATTAATAAATATTATAT
GTGATAAATCTAAATATGAACATTAGAAATCTGTGGGCACATATTTTTGCTGATTGGTT
AAAAAATTTTAAACAGGTCTTTAGCGTTCTAAGATATGCAAATGATATCTCTAGTTGTGAATT
TGTGATTAAAGTAAACCTTTTAGCTGTGTGTTCCCTTTACTTCTAATACTGATTTATGTTCT
AAGCCTCCCAAGTTCCAATGGATTGCGCTTCTCAAATGTACAACCTAAGCAACTAAAGAA
ATTAAGTGAAAGTTGAAAAAT

CGGAGTGGTGCGCCAACGTGAGAGGAAACCCGTGCGCGGCTGCGCTTTCCTGTCCCAAGCC

FIGURE 120

MLSESSSFLKGVMLGSIFCALITMLGHIRIGHGNRMHHEHHHLQAPNKEDILKISEDERME
LSKSFRVYCIILVKPKDVSLWAAVKETWTKHCDKAEFFSSENVKVFESINMDTNDMWLMMRK
AYKYAFDKYRDQYNWFFLARPTTFAI IENLKYFLKKDPSQPFYLGHTIKSGDLEYVGMEGG
IVLSVESMKRLNSLLNIPEKCPQQGGMIWKISEDKQLAVCLKYAGVFAENAEDADGKDVFNT
KSVGLSIKEAMTYHPNQVVEGCCSDMAVTFNGLTPNQMHVMMYGVYRLRAFGHIFNDALVFL
PPNGSDND

Signal sequence:

amino acids 1-33

N-glycosylation site.

amino acids 121-125, 342-346

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 319-323, 464-468

Casein kinase II phosphorylation site.

amino acids 64-132, 150-154, 322-326, 331-335, 368-372, 385-389,
399-403, 409-413, 473-477, 729-733, 748-752

Tyrosine kinase phosphorylation site.

amino acids 736-743

N-myristoylation site.

amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550,
558-564, 651-657, 657-663, 672-672

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 14-25

Cell attachment sequence.

amino acids 247-250

FIGURE 121

CCCACGCGTCCGATCTTACCAACAAAACACTCCTGAGGAGAAAGAAAGAGAGGGAGGGAGAG
AAAAAGAGAGAGAGAGAGAAAACAAAAACCAAAGAGAGAGAAAAAATGAATTCATCTAAATCAT
CTGAAACACAATGCACAGAGAGAGGATGCTTCTCTTCCCAAATGTTCTTATGGACTGTTGCT
GGGATCCCCATCCTATTTCTCAGTGCCTGTTTCATCACCAGATGTGTTGTGACATTTTCGCAT
CTTTCAAACCTGTGATGAGAAAAAGTTTCAGCTACCTGAGAATTTACAGAGCTCTCCTGCT
ACAATTATGGATCAGGTTCAGTCAAGAATTGTTGTCCATTGAACTGGGAATATTTTCAATCC
AGCTGCTACTTCTTTTCTACTGACACCATTTCTGGGCGTTAAGTTTAAAGAAGTCTCAGC
CATGGGGGCTCACCTGGTGGTTATCAACTCACAGGAGGAGCAGGAATTCCTTTCTACAAGA
AACCTAAAATGAGAGAGTTTTTATTGGACTGTCAGACCAGGTTGTGAGGGTCAGTGGCAA
TGGGTGGACGGCACACCTTTGACAAAGTCTCTGAGCTTCTGGGATGTAGGGGAGCCCAACAA
CATAGCTACCTGGAGGACTGTGCCACCATGAGAGACTCTTCAAACCCAAGGCCAAAATTGGA
ATGATGTAACCTGTTTCTCAATTATTTTCGGATTGTGAAATGGTAGGAATAAATCCTTGT
AACAAAGGAAAATCTCTTTAAGAACAGAAGGCACAACCTAAATGTGTAAAGAAGGAAGAGCA
AGAACATGGCCACCCCACCGCCCCACACGAGAAATTTGTGCGCTGAACTTCAAAGGACTTC
ATAAGTATTTGTTACTCTGATACAAATAAAAAATAAGTAGTTTAAATGTTAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAA

090572 071004
100725 223050

FIGURE 122

MNSSKSSETQCTERGCFSSQMFLWTVAGIPILFLSACFITRCVVTFRIFQTCDEKKFQLPEN
FTELSCYNYGSGSVKNCCLNWEYFQSSCYFFSTDTISWALSCLKNCAMGAHLVVINSQEEQ
EFLSYKKPKMREFFIGLSDQVVEGQWQWVDGTPLTKSLSFWDVGEPNNIATLEDCAIMRDSS
NPRQNWNDVTCFLNYFRICEMVGINPLNKGKSL

Signal sequence:

amino acids 1-42

N-glycosylation site.

amino acids 2-6, 62-66, 107-111

Casein kinase II phosphorylation site.

amino acids 51-55, 120-124, 163-167, 175-179, 181-185

N-myristoylation site.

amino acids 15-21, 74-80, 155-161

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 27-38

FIGURE 123

GGGACTACAAGCGCGCGCGCTGCCGCTGGCCCTCAGCAACCTCGACATGCGCGTGAGGCGGCCACCGCGAC
TCCGGCTCTGCGCTCGGCTGCCTGACTTCTTCCTGCTGCTGCTTTTCAGGGGCTGCTGATAGGGGCTGTAAATC
TCAATCCAGCAATCGAACCCAGTGGTACAGGAATTTGAAAGTGTGGAATCTGCTTCGATCATTACGGATTGCG
AGACAAGTGACCCAGGATCGAGTGGAGAAAATTCAGATGAAACAAACCATATGTGTTTTTGACAACAAA
TTCAGGGAGACTTGGCGGGTCGTGCAGAAATACTGGGGAAGACATCCCTGAAAGATCTGGAATGTGACACGGAGAG
ACTCAGCCCTTTATCGCTGTGAGGTCTGTGCTGAAATGACCGCAAGGAAATGTATGAGATTGTGATCGATTAA
CTGTGCTCAAGTGAAGCCACTGACCCCTGTCTGTAGAGTGCCGAAGGCTGTACCAATGAGGCAAGATGGCAACACTGC
ACTGCCAGGAGAGTGAGGGCCACCCCGGCCCTCACTACAGCTGGATCGCAATGATGTACCACTGCCACAGGATT
CCAGAGCCAAATCCAGATTTTCGCAATCTCTTTCCACTTAACTCTGAAACAGGCACTTTGGTGTTCACTGTGCT
TTCACAGGAGCACTCTGGGCAGTACTACTGCTTGTCCAAATGACCGAGGCTCAGCCAGGTGTGAGGAGCAGG
AGATGGAAGTCTATGACCTGAACATTTGGCGGAATTTATGGGGGGTTCTGGTGTGCTGTGTACTGGCCCTGTA
TCAGCTTGGGCATCTGTGCTGCATACAGACGTGGCTACTTCATCAACAATAAACAGGATGGAGAAAGTTACAAGA
ACCCAGGGAAACAGATGGAGTTAACTACATCCGCACTGACGAGGAGGGCGACTTCAGACACAGTCACTCTTTG
TGATCTGAGACCGCGGTGTGGCTGAGAGCGCAAGAGCGCACTGTCACATACCTCTCTGTAGAACTCCTGTCAA
GGCAGCGAGAGCTGATGCACTCGGACAGAGCTAGACACTTATTGAGAAGCTTTTCGTTTGGCCAAAGTTGACCA
CTACTCTTTACTCTAAACAGCCACATGAATAGAAGATTTTCTCAAGATGAGACCCGCTAAATATAACCAAA
GGAAGCGAAACTGGGTGCGTTCACTGAGTGGGTCTTAACTGTTTCTGGCCTGATTCGCCCATGAGTATTAGG
GTGATCTTAAAGAGTTTGCCTCAGCTAAACGCCGCTGTGGGCGCTGTGAAGCCAGCATGTTTACCACCTGGTCTGT
CAGCAGCCAGCAGCACACTGTGATGAGTGGCGAGGTGGCTGGACAGCAGCAGCGCATCCCGCGCGGAAACCCA
GAAAGCGCTTCTTACAGCAGCACTTACTTTCATCGGCCCAAGACCCGCGACTTCTCTTAAAGGGCTCTGC
TGATCGGTGTTTCAGTGTCCATTTGTGGAGAAGCTTTTGGATCAGCATTTGTAAAAACAACCAAAATCAGGAAG
GTAATTTGGTGTGCTGAGAGGGGATCTTGGCTGAGGAACCTGCTGTGACAGGGGTGTGAGGATTTAAGGAAA
ACCTTCGTCTTAGGCTAAGCTGAAATGGTACTGAAATATGCTTTTCTATGGGTCTTGTATTATTTATAAAATTT
TACATCTCAATTTTGTCAAGGATGATTTTGTATTATGAAAAGAAAATTTCTATTTTAAACTGTAATATATTGT
CATACATGTTAAATAACCTATTTTTTAAAAAAGTTCAACTTAAGGTAGAAGTTCAAGCTACTAGTGTATAAT
TGGAAAAATCAATAATTAAAGATTTTACCCAAAGGAATCCTCTCATGGAAGTTTACTGTGATTTCTTTCTTCT
CACACAAGTTTTCAGCTTTTTCACAAAGGAACTCATACTGTCTACACATCAGACCATAGTGTCTTAGGAAACCTT
TAAAAATTTCAAGTTAAAGCAATGTGAAATCAGTTTGCATCTCTTCAAAGAAACCTCTCAGGTAGCTTTGAACT
GCCTCTTCTCAGATGACTAGGACAGTCTGTACCCAGAGGCCACCCAGAAGCCCTCAGATGTACATACAGATG
CCAGTCAGCTCTCGGGTTTGGCCAGGCGCCCCGCTCTAGCTCACTGTTGCGCTGTGCTGACAGGAGGCCCT
GCCATCCTTGGGCCCTGGCAGTGGCTGTGCCAGTGAGCTTTACTCAGCTGGGCCCTGCTTCATCAGACAGC
TCTCAGGTGGGCACTGAGGGACACTGGTGTCTCCATGTAGCGTCCAGCTTTGGGCTCCTGTAACAGACCTCT
TTTTGGTTATGATGGCTCAAAAATAGGGCCCCCAATGCTATTTTTTTTTTTAAAGTTTGTTTAATTTATTTGTT
AAGATTGTCTAAGGCCAAAGGCCAATTGCGAAATCAAGTCTGTCAAGTACAATAACATTTTAAAGAAAATGGAT
CCCACTGTTCTCTTTGCCACAGAGAAAGCACCAGACGCCACAGGCTCTGTGCACTTTCAAACAAACCATGAT
GGAGTGGCGGCCACTCCAGCTTTTAAAGAACCTGAGTGGAGCAGCCAGGTGGAAGGCCCTGGCGAGGAGGAAG
TGAACGCGCTGAATCAAAGCAGTTTTCTAATTTTGACTTTAAATTTTTCATCCGCGGAGCACTGCTCCCATTT
TGTGGGGGACACTGACCAACTCACTCAGAAGCTGTGTTCTTCAAGAGCAGGTGCTCAGCCTCACATGGCCCT
CGCGTCTGGACTCAGGACTGAAGTGTGTAAGCAAGGAGTGTGAGAGGAGCACTCCACTGTGCTGGCTGGA
GAATGGCTCTCACTACTCACCTTGTCTTTCAGCTTCCAGTGTCTGGGTTTTTATATCTTTGACAGCTTTTTTT
AATGTGATACATGAGACTGTGTTGACTTTTTTAGTTTATGTGAACAACTTTGGCGCAGGCGCCCTGCGCAGGCA
GGAATGCTCTCAGCAGTGGCTCAGTGTCCCTGGTGTCTGCTGCAATGCACTCTGGAATGCTGTGCTGCTCAAGTTC
CCTCCATCATTGCCACTTTGGTAGAGAGGGATGGCTCCCAACCTCAGCGTGTGGGATTCAGCTCTCAGCCCTCT
TCTTGTGCTACATAGTAGAGGTAGCGCTTATTGCCCTCTTCTTATACCTAAACCTTCTACACTGATGGCCA
TGGGAACAGGCTCTGAAAAGTAGAGAGAAGTGAAGTAGAGTGTGGGAAGTAGCTGCTTAACTAGAGACTAGA
CGGAAAAGGAATCACTCGTGATTTTAAAGATATGAATGTGACTCAGACTCAGGCGCATCAGGCTGTGATTTCT
GCCTTTGGATGGATGTTGCTGTACACAGTGTACAGACTTGTACTAACACACCGTAATTTGGCATTTGTTTAACT
CTCATTTATAAAGCTTCAAAAAACCA

FIGURE 124

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77624
><subunit 1 of 1, 310 aa, 1 stop
><MW: 35020, pI: 7.90, NX(S/T): 3
MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRPVQEFESVELSCIITDSQTS
PRIEWKKIQDEQTTVVFNDNKIQGDLAGRAEILGKTSKLIWNVTRDSALYRCEVVARNDRK
EIDEIVIELTVQVKPVTVPVCRVPKAVPVGKMATLHCQSEGHPRPHYSWYRNDVPLPTDSRA
NPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEYVDLNIIGGIIG
VLVVLAVLALITLIGICCAYYRRGYFINNKQDGESYKNPGKPDGVNYYIRTDEEGDFRHKSSFVI
```

Important features of the protein:

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 243-263

N-glycosylation sites.

amino acids 104-107, 192-195

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 107-110

Casein kinase II phosphorylation site.

amino acids 106-109, 296-299

Tyrosine kinase phosphorylation site.

amino acids 69-77

N-myristoylation sites.

amino acids 26-31, 215-220, 226-231, 243-248, 244-249, 262-267